

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: July 7, 2005, 14:30:40 ; Search time 76 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150

Sequence: 1 QARONLQNLPLNFICLLICLLICILVWL 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir79: *
2: pir1: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	100.0	52	A29002	phospholamban - do
2	150	100.0	52	A49057	phospholamban - mo
3	150	100.0	52	B40424	phospholamban - ra
4	150	100.0	52	S05540	phospholamban - pl
5	150	100.0	52	S37638	phospholamban - ra
6	144	96.0	52	A40424	phospholamban - hu
7	137	91.3	52	A39535	phospholamban - ch
8	58.5	39.0	305	T34299	hypothetical prote
9	57	38.0	169	A81455	probable integral
10	55	36.7	669	T08827	hypothetical prote
11	53	35.3	431	B97277	probable O-antigen
12	53	35.3	573	I40496	methylation enzyme
13	53	35.3	1880	T18531	cractin - medicina
14	52.5	35.0	77	1MNIH3	nonstructural prot
15	52.5	35.0	77	S25709	hypothetical prote
16	52	34.7	80	T28256	ORF MSV095 hypote
17	52	34.7	354	T2319	hypothetical prote
18	52	34.7	382	T41256	hypothetical rymo
19	52	34.7	396	AH1421	efflux protein hom
20	52	34.7	1014	H71602	protein with dnuv
21	52	34.7	1182	T13952	membrane protein p
22	51	34.0	458	F86433	protein T17H7.5 (l
23	51	34.0	584	JC7809	sulfakinin recepto
24	50.5	33.7	858	JC7683	taste receptor T1R
25	50.5	33.7	177	B70156	probable chromate
26	50.5	33.7	388	C81568	hypothetical prote
27	50.5	33.7	388	H86520	hypothetical prote
28	50	33.3	211	B56691	mpal 5'-region hyp
29	50	33.3	226	JQ1570	major surface anti

30	50	33.3	226	2	JQ2058	surface antigen -
31	50	33.3	226	2	JQ2061	surface antigen -
32	50	33.3	226	2	JQ2060	surface antigen -
33	50	33.3	226	2	JQ2057	surface antigen -
34	50	33.3	226	2	JQ2062	surface antigen -
35	50	33.3	226	2	JQ2059	surface antigen -
36	50	33.3	348	2	JC7907	common cytokine re
37	50	33.3	359	2	B59105	hypothetical prote
38	50	33.3	378	2	T34372	hypothetical prote
39	50	33.3	388	2	E72103	hypothetical prote
40	50	33.3	389	1	SAVLJ1	large surface anti
41	50	33.3	389	1	SAVLJ2	large surface anti
42	50	33.3	389	1	SAVLJ3	large surface anti
43	50	33.3	484	2	C88264	protein kin-15 (lm
44	50	33.3	488	2	I44330	protein-tyrosine k
45	50	33.3	511	2	F86460	probable cytochrom

ALIGNMENTS

RESULT 1
A29002
phospholamban - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A29002; A26805; A25307; A24818; I46227
R:Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M.
U. Clin. Invest. 75, 301-304, 1987
A:Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phospholamban
A:Reference number: A29002; MUID:87083954; PMID:3793929
A:Accession: A29002
A:Molecule type: mRNA
A:Residues: 1-52 <RUI>
A:Cross-references: UNIPROT:P61012; GB:M16012; NID:g164043; PIND:AAA30884.1; PID:g164044
R:Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Res. 15, 6738, 1987
A:Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular muscle
A:Reference number: A26805; MUID:87316936; PMID:3628007
A:Accession: A26805
A:Molecule type: mRNA
A:Residues: 1-52 <YBE>
A:Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912
R:Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R.
J. Biol. Chem. 261, 13333-13341, 1986
A:Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and
A:Reference number: A25307; MUID:87008549; PMID:3759968
A:Contents: partial sequence and phosphorylation sites
A:Accession: A25307
A:Molecule type: protein
A:Residues: 10-45 <SIM>
R:Fujii, J.; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F.
Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986
A:Title: Characterization of structural unit of phospholamban by amino acid sequencing
A:Reference number: A24818; MUID:86323152; PMID:3753485
A:Contents: partial sequence and acetylation site
A:Accession: A24818
A:Molecule type: protein
A:Residues: 1-35, 'X', 37-40, 'X', 42-45 <FUI>
R:Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Symp. Ser. 17, 121-124, 1986
A:Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
A:Reference number: I46227; MUID:87174660; PMID:356256
A:Accession: I46227
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-52 <UY2>
A:Cross-references: GB:M35393; NID:g164045; PIDN:AA41618.1; PID:g164046
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, ar
e, after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; ti

F:31-52/Domain: transmembrane #status predicted <TM>
 F:1/Modified site: acetylated amino end (Met) #status experimental
 F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status experiment
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status experiment

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QARONLQNLFINFCILICLLICITIVML 30
 Db 23 QARONLQNLFINFCILICLLICITIVML 52

RESULT 2

A49057
 phospholamban - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: A49057

R:Ganim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.;
 Circ. Res. 71, 1021-1030, 1992

A:Title: Mouse phospholamban gene expression during development in vivo and in vitro.
 A:Reference number: A49057; MUID:93008602; PMID:1394867

A:Accession: A49057
 A:Molecule type: mRNA

A:Cross-references: UNIPROT:P61014; GB:S46792; NID:9257745; PIDN:AA23706.1; PID:9257746

A:Experimental source: cardiac muscle
 A>Note: Sequence extracted from NCBI backbone (NCBI:116999, NCBI:P117001)

C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
 e: after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is

C:Superfamily: cardiac phospholamban
 C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr

F:31-52/Domain: transmembrane #status predicted <TM>
 F:1/Modified site: acetylated amino end (Met) #status predicted

F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QARONLQNLFINFCILICLLICITIVML 30
 Db 23 QARONLQNLFINFCILICLLICITIVML 52

RESULT 3

B40424
 phospholamban - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: B40424; S00249

R:Fujii, J.; Zairain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.
 J. Biol. Chem. 266, 11659-11675, 1991

A:Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and asse
 A:Reference number: A40424; MUID:91268032; PMID:1828805

A:Accession: B40424
 A:Molecule type: DNA

A:Residues: 1-52 <FUS>
 A:Cross-references: UNIPROT:P61015; GB:M63601; NID:9165636; PIDN:AAA1445.1; PID:9165639

R:Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.
 FEBS Lett. 227, 51-55, 1988

A:Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene.
 A:Reference number: S00249; MUID:88112222; PMID:2962883

A:Accession: S00249
 A:Status: not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 1-52 <FUS>

A:Cross-references: GB:Y00761; NID:91661; PIDN:CAA68730.1; PID:91662
 C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and

C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplasm
 e: after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is

A>Note: only one gene was detected
 A:Note: the single intron is upstream of the coding region

C:Superfamily: cardiac phospholamban
 C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr

F:31-52/Domain: transmembrane #status predicted <TM>
 F:1/Modified site: acetylated amino end (Met) #status predicted

F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QARONLQNLFINFCILICLLICITIVML 30
 Db 23 QARONLQNLFINFCILICLLICITIVML 52

RESULT 4

S05540
 phospholamban - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: S05540

R:Verboom, H.; Muytack, F.; Eggermont, J.A.; de Jaegere, S.; Misslaen, L.; Raeymaekers
 Biochem. J. 262, 353-356, 1989

A:Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.
 A:Reference number: S05540; MUID:90056437; PMID:2530978

A:Accession: S05540
 A:Molecule type: mRNA

A:Cross-references: UNIPROT:P61013; EMBL:X15075; NID:92055; PIDN:CAA33171.1; PID:92056

C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and
 e: after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation is

C:Superfamily: cardiac phospholamban
 C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr

F:31-52/Domain: transmembrane #status predicted <TM>
 F:1/Modified site: acetylated amino end (Met) #status predicted

F:16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QARONLQNLFINFCILICLLICITIVML 30
 Db 23 QARONLQNLFINFCILICLLICITIVML 52

RESULT 5

S37638
 phospholamban - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Mar-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: S37638; I52270; I64795; I51940

R:Shanahan, C.M.; Weisberg, F.U.; Metcalfe, J.C.
 Circ. Res. 73, 193-204, 1993

A:Title: Isolation of gene markers of differentiated and proliferating vascular smooth m
 A:Reference number: S37637; MUID:93284726; PMID:8508530

A:Accession: S37638
 A:Molecule type: mRNA

A:Residues: 1-52 <SHA>
 A:Cross-references: UNIPROT:P61016; EMBL:X71068; NID:9313809; PIDN:CAA50394.1; PID:93138

R:Johns, D.C.; Feldman, A.M.
 Biochem. Biophys. Res. Commun. 189, 927-933, 1992

A:Title: Identification of a highly conserved region at the 5' flank of the phospholamban
 A:Reference number: I52270; MUID:93075183; PMID:1445334

A:Accession: I52270

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A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-52 <J0H>
A:Cross-references: GB:103382; NID:g206134; PION:AAA1849.1; PID:g206136
R:Wang, K.S.; Nadal-Ginard, B.
Adv. Exp. Med. Biol. 304, 387-395, 1991
A>Title: Cloning phospholamban cDNA from rat aortic smooth muscle.
A:Reference number: 151840; MUID:92206263; PMID:1725098
A:Accession: 164795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HMA1>
A:Cross-references: GB:S95853; NID:g247932; PIDN:AAB21903.1; PID:g247933
A:Accession: 151840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HMA2>
A:Cross-references: GB:S95849; NID:g247934
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
Pase; after phosphorylation, the calcium pump is activated and the rate of muscle relaxa
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; pho
F:31-52/Domain: transmembrane #status predicted <TMM>
F:16/Binding site: acetylated amino end (Met) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 100.0%; Score 150; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 2,9e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 23 QARQNLQNLFINFCILICLLICILIVML 52

RESULT 6
A40424
phospholamban - human
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
A:Accession: A40424
R:Fujii, J.; Zaratin-Herzberg, A.; Willard, H.F.; Tade, M.; MacLennan, D.H.
J. Biol. Chem. 266, 11659-11675, 1991
A>Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and asse
A:Reference number: A40424; MUID:91268032; PMID:1828805
A:Accession: A40424
A:Molecule type: mRNA
A:Residues: 1-52 <F0J>
A:Cross-references: UNIPROT:P26678; GB:M63603; NID:g189942; PION:AAA6083.1; PID:g189943
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Comment: Helical transmembrane domains of five chains are thought to aggregate in the
C:Genetics:
A:Gene: GDB:PLN; PUB
A:Cross-references: GDB:128300; OMIM:172405
A:Map position: 6q22.1-6q22.1
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:31-52/Domain: transmembrane #status predicted <TMM>
F:16/Binding site: acetylated amino end (Met) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 96.0%; Score 144; DB 1; Length 52;
Best Local Similarity 96.7%; Pred. No. 1.5e-11;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 QARQNLQNLFINFCILICLLICILIVML 30
23 QARQNLQNLFINFCILICLLICILIVML 52

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RESULT 7
A39535
phospholamban - chicken
C:Species: Gallus gallus (chicken)
C>Date: 06-Mar-1992 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A39535; B39535; A44531
R:Toyofuku, T.; Zak, R.
J. Biol. Chem. 266, 5375-5383, 1991
A>Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban
A:Reference number: A39535; MUID:91170195; PMID:1825996
A:Accession: A39535
A:Molecule type: mRNA
A:Residues: 1-117; 119-52 <TOY>
A:Cross-references: UNIPROT:P26677; GB:M59039; NID:g212575; PION:AAA62738.1; PID:g212576
A:Note: the authors translated the codon CTT for residue 18 as Ile
A:Accession: B39535
A:Molecule type: DNA
A:Residues: 1-52 <TO2>
A:Cross-references: GB:M59038
A:Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not
R:Toyofuku, T.; Zak, R.
submitted to Genbank, April 1991
A:Reference number: A44531
A:Accession: A44531
A:Molecule type: DNA
A:Residues: 1-52 <TO3>
A:Cross-references: GB:M59038
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Genetics:
A:Note: only one gene was detected
A:Note: the single intron is upstream of the coding region
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:31-52/Domain: transmembrane #status predicted <TMM>
F:16/Binding site: acetylated amino end (Met) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 91.3%; Score 137; DB 1; Length 52;
Best Local Similarity 90.0%; Pred. No. 9.9e-10;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 1 QARQNLQNLFINFCILICLLICILIVML 30
23 QARQNLQNLFINFCILICLLICILIVML 52

RESULT 8
T34299
hypothetical protein F54E7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A:Accession: T34299
R:Bentley, D.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of C. elegans cosmid F54E7.
A:Reference number: 221502
A:Accession: T34299
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-305 <BEN>
A:Cross-references: UNIPROT:Q20783; EMBL:U00067; PION:AACT7517.1; GSPDB:GN00021; CESP:F5
A:Experimental source: strain Bristol N2; clone F54E7
C:Genetics:
A:Gene: CESP:F54E7.5
A:Map position: 3
A:Introns: 78/3; 173/3
Query Match 39.0%; Score 58.5; DB 2; Length 305;

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Best Local Similarity 54.2%; Pred. No. 6;
Matches 13; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
Oy 7 ONLFINFCLILICLIIVML 30
Db 186 QHLLI-ACLILICLTFTTFFI 208

RESULT 9
AB1445
probable integral membrane protein Cj0266c [imported] - Campylobacter jejuni (strain NCTC)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
A:Accession: AB1445
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Baaham, D.; Chilling
C.W.; Quail, M.; Rajadaram, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: AB1445
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <PAR>
A:Cross-references: UNIPROT:O9PTM9; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7273
A:Experimental source: serotype O2, strain NCTC 1168
C:Genetics:
A:Gene: Cj0266c
C:Superfamily: Campylobacter jejuni probable integral membrane protein Cj0266c

Query Match 38.0%; Score 57; DB 2; Length 169;
Best Local Similarity 52.6%; Pred. No. 5.8;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Oy 11 INFCLILICLIIVML 29
Db 9 IAFILICFALICLIIFL 27

RESULT 10
T08827
hypothetical protein cotel - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T08827
R:Wiffield, S.L.; Tayebi, N.; Martin, B.M.; Gimn, E.I.; Sidransky, E.
Genome Res. 7, 1020-1026, 1997
A:Title: Identification of three additional genes contiguous to the glucocerebrosidase 1
A:Reference number: Z16482; MUID:97474796; PMID:9331372
A:Accession: T08827
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-669 <WIN>
A:Cross-references: UNIPROT:P81408; EMBL:AF023266; NID:g5564910; PIDN:AMC51822.1; PID:g2
C:Genetics:
A:Gene: cotel
A:Map position: 1
A:introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1; 505/1; 528/1; 612/3

Query Match 36.7%; Score 55; DB 2; Length 669;
Best Local Similarity 38.5%; Pred. No. 27;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
Oy 1 QARQNLQNLFTNFCILICLIICII 26
Db 165 EARGALKLRLSVCLITCAITCRL 190

RESULT 11
B97277
probable O-antigen/teichoic acid transporter CAC3065 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97277

R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
. J. Daily, M.C.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97277
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-431 <KUN>
A:Cross-references: UNIPROT:Q9TEP3; GB:AE001437; PIDN:AAK81005.1; PID:g15026127; GSPDB:G
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3065
C:Superfamily: O-antigen transporter protein

Query Match 35.3%; Score 53; DB 2; Length 431;
Best Local Similarity 32.1%; Pred. No. 34;
Matches 9; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Oy 3 QNLQNLFTNFCILICLIIVML 30
Db 83 KKIEIFNSVMLIKALITICFIIVMLV 110

RESULT 12
140496
methylacton enzyme tIpc - Bacillus subtilis
N:Alternate names: 62k MCP-like protein TIPC; methyl-accepting chemotaxis protein tIpc
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: 140496; B69724; E45067
R:Hanlon, D.W.; Rosario, M.W.; Ordal, G.W.; Venema, G.; Van Sinderen, D.
Microbiology 140, 1847-1854, 1994
A:Title: Identification of TIPC, a novel 62 kDa MCP-like protein from Bacillus subtilis.
A:Reference number: 140495; MUID:95005439; PMID:7921238
A:Accession: 140496
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-573 <RES>
A:Cross-references: UNIPROT:P39209; EMBL:Z34005; NID:g496483; PIDN:CAA83970.1; PID:g4964
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Eutchan, K.D.; Errington, D.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler
Jech, J.; Harwood, C.R.; Henauc, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koster, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lamber, U.J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69724
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-215, 'T', 217-331, 'P', 333-573 <KUN>
A:Cross-references: GB:Z59105; GB:AL009126; NID:g2632457; PIDN:CAB12138.1; PID:g2632630
A:Experimental source: strain 168
C:Genetics:
A:Gene: tIpc
C:Superfamily: methyl-accepting chemotaxis protein

Query Match 35.3%; Score 53; DB 2; Length 573;
Best Local Similarity 29.2%; Pred. No. 42;
Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Oy 7 ONLFINFCLILICLIIVML 30
Db 183 QSLTFQFAIVLIVIMSVILVLV 206

RESULT 13

T18531

tractin - medicinal leech

C:Species: Hirudo medicinalis (medicinal leech)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18531

R: Huang, Y.; Jellies, J.; Johansen, K.M.; Johansen, J.

J. Cell Biol. 138, 143-157, 1997

A:Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-superfamily me

A:Reference number: Z18951; MUID:97362067; PMID:9214388

A:Accession: T18531

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1880 <HNA>

A:Cross-references: UNIPROT:O18465; EMBL:U92813; NID:G2275259; PID:G2275260; PIDN:AAC476

Query Match

Best Local Similarity 35.3%; Score 53; DB 2; Length 1880;

Matches 8; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 12 NPLILICLLICIIIVML 30

DB 1751 NWLILICLLILLLIL 1769

RESULT 14

NM1H3

nonstructural protein 5B - human coronavirus (strain 229E)

C:Species: human coronavirus

C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C:Accession: C34038

R: Raabe, T.; Siedell, S.

Nucleic Acids Res. 17, 6387, 1989

A:Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique

A:Reference number: A34038; MUID:8936667; PMID:2701946

A:Accession: C34038

A:Molecule type: genomic RNA

A:Residues: 1-77 <RAA>

A:Cross-references: UNIPROT:P19741; EMBL:X15654; NID:G58921; PIDN:CAA33684.1; PID:G58925

C:Superfamily: coronavirus nonstructural protein 5B

C:Keywords: nonstructural protein

Query Match

Best Local Similarity 35.0%; Score 52.5; DB 1; Length 77;

Matches 10; Conservative 8; Mismatches 4; Indels 3; Gaps 1;

QY 9 LFIN---FCLILICLLICIIIVML 30

DB 11 LVNVVLMWCVLIVILVCIITIKL 35

RESULT 15

S25709

hypohectical protein 5 - human coronavirus

C:Species: human coronavirus 229E

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jul-2001

C:Accession: S25709

R: Jouveine, P.; Mounir, S.; Stewart, J.N.; Richardson, C.D.; Talbot, P.J.

Virus Res. 22, 125-141, 1992

A:Title: Sequence analysis of human coronavirus 229E mRNAs 4 and 5: evidence for polymor

A:Reference number: S25708; MUID:9230395; PMID:1373555

A:Accession: S25709

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-77 <YOU>

A:Cross-references: EMBL:X64942; NID:G59462; PIDN:CAA46114.1; PID:G59464

C:Superfamily: coronavirus nonstructural protein 5B

Query Match

Best Local Similarity 35.0%; Score 52.5; DB 2; Length 77;

Matches 10; Conservative 8; Mismatches 4; Indels 3; Gaps 1;

QY 9 LFIN---FCLILICLLICIIIVML 30
 DB 11 LVNVVLMWCVLIVILVCIITIKL 35

Search completed: July 7, 2005, 15:42:30
 Job time : 77 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:19:31 ; Search time 394 Seconds
(without alignments)

38,991 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150

Sequence: 1 QARONLQNLFINFCILICLLICIVML 30

Scoring table: BLOSUM62

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150	100.0	52	1 PPLA_CANFA	P61012 canis fam1
2	150	100.0	52	1 PPLA_MOUSE	P61014 mus musculu
3	150	100.0	52	1 PPLA_PIG	P61013 sus scrofa
4	150	100.0	52	1 PPLA_RABIT	P61016 oryctolagus
5	150	100.0	52	1 PPLA_RAT	P61016 ratcus norv
6	144	96.0	52	1 PPLA_HUMAN	P26677 homo sapien
7	137	91.3	52	1 PPLA_CHICK	P26677 gallus gall
8	59.5	39.7	792	2 Q07816	Q07816 caenorhabd
9	58.5	39.0	305	2 Q20783	Q20783 mus musculu
10	58	38.7	31	1 SARL_MOUSE	Q9cqd6 mus musculu
11	58	38.7	31	2 Q6SLB7	Q6SLB7 ratcus norv
12	57.5	38.3	130	2 Q70V94	Q70V94 cotesia kaz
13	57	38.0	169	2 Q9PIM9	Q9PIM9 campylobact
14	56	37.3	35	2 Q6VZB7	Q6VZB7 bidesodes
15	56	37.3	110	2 Q8BS41	Q8BS41 mus musculu
16	56	37.3	268	2 Q801W9	Q801W9 equash leat
17	56	37.3	357	2 Q8EWJ5	Q8EWJ5 mycoplasma
18	56	37.3	422	1 K3L1_RAT	P83556 ratcus norv
19	56	37.3	4638	2 Q8IKS6	Q8IKS6 plasmodium
20	55.5	37.0	130	2 Q70V90	Q70V90 cotesia oro
21	55.5	37.0	218	2 Q6ER12	Q6ER12 cotesia oro
22	55.5	37.0	400	2 Q8DKW1	Q8DKW1 streptococc
23	55.5	37.0	400	2 Q8EB10	Q8EB10 streptococc
24	55	36.7	31	1 SARL_HUMAN	Q00631 homo sapien
25	55	36.7	122	2 Q8R0C6	Q8R0C6 mus musculu
26	55	36.7	364	2 Q896T0	Q896T0 clostridium
27	55	36.7	369	2 Q8L1E8	Q8L1E8 bacillus an
28	55	36.7	394	2 Q6H078	Q6H078 bacillus an
29	55	36.7	668	2 Q9BR66	Q9BR66 homo sapien
30	55	36.7	669	1 COTE_HUMAN	P81408 homo sapien
31	54	36.0	326	2 Q6GN07	Q6GN07 xenopus lae

32	54	36.0	433	1 PIGU_MOUSE	Q8K358 mus musculu
33	54	36.0	434	1 PIGU_HUMAN	Q9H490 homo sapien
34	54	36.0	434	1 PIGU_RAT	Q8CHJ1 ratcus norv
35	54	36.0	482	2 Q9MGA9	Q9MGA9 chrysothidym
36	54	36.0	513	2 Q67SR3	Q67SR3 oikopleura
37	54	36.0	720	2 Q40902	Q40902 pecunia inc
38	53.5	35.7	130	2 Q70V97	Q70V97 cotesia fla
39	53.5	35.7	217	2 Q6ER08	Q6ER08 cotesia mel
40	53.5	35.7	217	2 Q6EF10	Q6EF10 cotesia mel
41	53	35.3	113	2 Q8C8J2	Q8C8J2 mus musculu
42	53	35.3	245	2 Q7SME1	Q7SME1 ovine enzoo
43	53	35.3	245	2 Q7SME2	Q7SME2 ovine enzoo
44	53	35.3	263	2 Q92SD4	Q92SD4 ratcus norv
45	53	35.3	263	2 Q9WU52	Q9WU52 mus musculu

ALIGNMENTS

RESULT 1
PPLA_CANFA STANDARD; PRT; 52 AA.
ID PPLA_CANFA
AC P61012; P07473; 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name=PLN;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_Taxid=9615;
RN [1]
RP MEDLINE=87083954; PubMed=3793929;
RA Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Toda M.,
RT "Complete complementary DNA-derived amino acid sequence of canine
RT cardiac phospholamban.";
RL J. Clin. Invest. 79:301-304(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart ventricle;
RX MEDLINE=87316936; PubMed=3628007;
RA Uyeda A., Kitano K., Fujii J., Kadoma M., Toda M., Tanaka S.;
RT "The cDNA sequence of the major phospholamban mRNA in canine cardiac
RT ventricular muscle.";
RL Nucleic Acids Res. 15:6738-6738(1987).
RN [3]
RP SEQUENCE OF 1-45, AND ACETYLATION.
RX MEDLINE=86323152; PubMed=3753485;
RA Fujii J., Kadoma M., Toda M., Tanaka S.,
RT "Characterization of structural unit of phospholamban by amino acid
RT sequencing and electrophoretic analysis.";
RL Biochem. Biophys. Res. Commun. 138:1044-1050(1986).
RN [4]
RP SEQUENCE OF 10-45, AND PHOSPHORYLATION SITES SER-16 AND THR-17.
RX MEDLINE=87008549; PubMed=3759968;
RA Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
RA Jones L.R.;
RT "Sequence analysis of phospholamban. Identification of phosphorylation
RT sites and two major structural domains.";
RL J. Biol. Chem. 261:13333-13341(1986).
RN [5]
RP PHOSPHORYLATION SITES SER-16 AND THR-17.
RX MEDLINE=89291905; PubMed=2544595;
RA Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.;
RT "Phospholamban phosphorylation in intact ventricles. Phosphorylation
RT of serine 16 and threonine 17 in response to beta-adrenergic
RT stimulation.";
RL J. Biol. Chem. 264:11468-11474(1989).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcolemmal reticulum.
CC -1- SUBUNIT: Homopentamer.

```
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
-----
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CC -----
DR EMBL M16012; AAA30884.1; -.
DR EMBL Y00399; CAA68461.1; -.
DR EMBL M35393; AAC41618.1; -.
DR PIR A29002; A29002.
DR InterPro IPR005984; Pfam 1.
DR PIRSF PIRSF001665; PLB; 1.
DR TIGRFAMs TIGR01294; P_lamban; 1.
KM Acetylation; Direct protein sequencing; Phosphorylation; Transmembrane.
KW DOMAIN 1 31 Cytoplasmic (Potential).
FT FT TRANSMEM 32 52 Potential.
FT MOD_RES 1 1 N-acetylmethionine.
FT MOD_RES 16 16 Phosphoserine (by PKA).
FT MOD_RES 17 17 Phosphothreonine (by CaMKII).
SQ SEQUENCE 52 AA; 6080 MW; 07631D9ADC424D3 CRC64;

Query Match 100.0%; Score 150; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.2e-10; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 2
PEPLA_MOUSE STANDARD; PRT; 52 AA.
ID ID P61014; P20006;
AC AC 01-FEB-1991 (Rel. 17, Created)
DT DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE DE Cardiac phospholamban (PLB).
GN GN Name=Pln;
OS OS Mus musculus (Mouse).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX OX NCBI_TaxId=101090;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RC RC TISSUE=Heart;
RX RX MEDLINE=93008802; PubMed=1394867;
RA RA Ganun J.R., Luo W., Pomlath S., Grupp I., Kim H.W., Ferguson D.G.,
RA Kadambi V., Neumann J.C., Doetschman T., Kianias E.G.;
RT RT "Mouse phospholamban gene expression during development in vivo and in vitro.";
RL RL Circ. Res. 71:1021-1030(1992).
RN RN [2]
RP RP SEQUENCE FROM N.A.
RX RX STRAIN=C57BL/6J; TISSUE=Aorta, Heart, and Kidney;
RX RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA RAKasaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nitaiido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldaralli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schimml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Choithia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D.,
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RA Kanai A, Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan M.J., Petrea G., Pesole G.,
RA Petrovsky N., Piliat R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravaei T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shmida K.,
RA Sultana R., Taketaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vetrardo R., Wagner L., Walstedt C., Wang Y., Waranabe Y., Wells C.,
RA Wilming L.G., Wysshaw-Bois A., Yangisawa M., Yang I., Yang L.,
RA Yun Z., Zavalan M., Zhu Y., Zimmer A., Zirinchi P., Hayatsu N.,
RA Hirozane-Kishikawa T., Komito H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino Y., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603892;
RC Strausberg R.L., Fellings F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dichtchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsuki S., Carinini P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcooplasmic reticulum.
CC -1- SUBUNIT: Homopentamer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation (By
CC similarity).
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, S46792; AAB23706.1; -
DR EMBL, AK002622; BAB22237.1; -
DR EMBL, AK040718; BAC30680.1; -
DR EMBL, AK052199; AAC34880.1; -
DR EMBL, BC061097; AAB61097.1; -
DR PIR, A49057; A49057.
DR HSSP, P07473, 1BYK.
DR WGD, WGI:97622, PIN.
DR InterPro, IPR005984, P_Lamban.
DR PIRSF, PIRSF001665, PLB, 1.
DR TIGRFAMs, TIGR01294, P_Lamban; 1.
KW Acetylation; Phosphorylation; Transmembrane.
FT DOMAIN 1 31 Cytoplasmic (Potential).
FT

FT	TRANSMEM	32	52	Potentail.
FT	MOD_RES	1	1	N-acetylmetionine (By similarity).
FT	MOD_RES	16	16	Phosphoserine (by PKA) (By similarity).
FT	MOD_RES	17	17	Phosphothreonine (by CamK) (By similarity).
FT	SEQUENCE	52 AA;	6094 MW;	0763601F76A854D3 CRC64;
SQ				
Query Match		100.0%;	Score 150;	DB 1; Length 52;
Best local Similarity		100.0%;	Pred. No. 1.2e-10;	
Matches	30; Conservative	0;	Mismatches	0; Indels 0; Gaps 0
Oy	1	QARONLQMLFIINFCILICLLICLIYVWLL	30	
Dd	23	QARONLQMLFIINFCILICLLICLIYVWLL	52	
RESULT 3				
PPLA_PIG	ID	STANDARD;	PRT;	52 AA.
AC	P610I3, P07473;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-APR-1988 (Rel. 07, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cardiac phospholamban (PLB).			
GN	Name=PLN;			
OS	Sw sacrota (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_Taxid=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Smooth muscle;			
RA	MEDLINE=90056437; PubMed=2530978;			
RA	Veddoomen H., Wuytsack F., Eggermont J.A., de Jaegere S., Misseisen L., Raeymaekers L., Casceels R.;			
RT	"cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.";			
RL	Biochem. J. 262:353-356(1989).			
RN	[2]			
RP	STRUCTURE BY NMR.			
RA	Lamberth S., Grlesinger C., Schmid H., Carafoll E., Muenchbach M., Vorherr T., Krebs J.;			
RT	"NMR solution structure of phospholamban membrane protein.";			
RL	Submitted (Aug-2000) to the PDB data bank.			
CC	-1- FUNCTION: Phospholamban has been postulated to regulate the activity of the calcium pump of cardiac sarcoplasmic reticulum.			
CC	-1- SUBUNIT: Homopentamer (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Membrane (By similarity).			
CC	-1- PTM: Phosphorylated in response to beta-adrenergic stimulation (By similarity).			
CC	-1- SIMILARITY: Belongs to the phospholamban family.			
CC	-----			
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CC	-----			
DR	EMBL, X15075; CAJ33171.1; .			
DR	PIR, S05540; S05540.			
DR	PDB, 1FJK; NMR, .			
DR	InterPro, IPR005984; P lamban.			
DR	PIRSF, PIRSF001665; PLB; 1.			
DR	TIGRFAMs, TIGR01294; P_lamban; 1.			
KW	3D-structure; Acetylation; Phosphorylation; Transmembrane.			
FT	DOMAIN	1	31	Cytosolic (Potential).
FT	TRANSMEM	32	52	Potentail.
FT	MOD_RES	1	1	N-acetylmetionine (By similarity).
FT	MOD_RES	16	16	Phosphoserine (by PKA) (By similarity).
FT	MOD_RES	17	17	Phosphothreonine (by CamK) (By similarity).
FT	MOD_RES	17	17	Phosphochreonine (by CamK) (By similarity).
FT				

FT	HELIX	4	16
FT	HELIX	21	49
FT	TURK	50	52
SO	SEQUENCE	52 AA; 6080 MW; 076361D9ADC42AD3 CRC64;	
Oy	1 QARONLQNLFINCLILICLLILCIYML 30		
Dh	23 QARONLQNLFINCLILICLLILCIYML 52		
	Query Match	100.0%; Score 150; DB 1; Length 52;	
	Best Local Similarity	100.0%; Pred. No. 1.2e-10;	
	Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
	RESULT 4		
	PPLA_RABIT STANDARD; PRT; 52 AA.		
ID	PPLA_RABIT		
AC	P61015; P20006;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DE	25-OCT-2004 (Rel. 45, Last annotation update)		
DR	Cardiac phospholamban (PLB).		
GN	Name=PLN;		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91268032; PubMed=1828805;		
RA	Fujii J., Zarehi-Hertzberg A., Willard H.F., Tada M., MacLennan D.H.;		
RT	"Structure of the rabbit phospholamban gene, cloning of the human		
RL	cDNA, and assignment of the gene to human chromosome 6."		
RL	J. Biol. Chem. 266:11669-11675(1991).		
RP	[2]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=88112222; PubMed=2962883; DOI=10.1016/0014-5793(88)81412-1;		
RA	Fujii J., Lytton J., Tada M., MacLennan D.H.;		
RT	"Rabbit cardiac and slow-twitch muscle express the same phospholamban		
RL	gene."		
RL	FEBS Lett. 227:51-55(1988).		
CC	-I- FUNCTION: Phospholamban has been postulated to regulate the		
CC	activity of the calcium pump of cardiac sarcoplasmic reticulum.		
CC	-I- SUBUNIT: Homopentamer.		
CC	-I- SUBCELLULAR LOCATION: Membrane.		
CC	-I- TISSUE SPECIFICITY: Heart.		
CC	-I- PTM: Phosphorylated in response to beta-adrenergic stimulation.		
CC	-I- SIMILARITY: Belongs to the phospholamban family.		
CC	-----		
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CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; M63600; -; NOT ANNOTATED_CDS.		
DR	EMBL; M63601; AAA11445.1; -;		
DR	EMBL; Y00761; CAA68730.1; -;		
DR	PIR; B40424; B40424.		
DR	HSSP; P07473; IEVK.		
DR	INAC; P61015; -.		
DR	InterPro; IPR005984; P_lamban.		
DR	PIRSF; PIRSF001665; PLB; 1.		
DR	TIGRFAMs; TIGR01294; P_lamban.1.		
KW	Acetylation; Phosphorylation; Transmembrane.		
FT	DOMAIN 1 31		
FT	TRANSMEM 32 52		
FT	MOD_RES 1 1		
FT	MOD_RES 16 16		
FT	MOD_RES 17 17		
FT	Cytoplasmic (Potential).		
FT	N-acetylmetionine (By similarity).		
FT	Phosphoserine (by PKC) (By similarity).		
FT	Phosphothreonine (by CaMK) (By		
FT	similarity).		


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RX MEDLINE=95298769; PubMed=7779806;
RA Morfienre-Smith R.J., Pitzemberger S.M., Burke C.J., Midaugh C.R.,
RA Garaky V.M., Johnson R.G.;
RT "Solution structure of the cytoplasmic domain of phospholamban:
RT phosphorylation leads to a local perturbation in secondary
RT structure."
RN Biochemistry 34:7603-7613(1995).
RL [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95269058; PubMed=7749920;
RA Adams P.D., Atkin I.T., Engelman D.M., Bruenger A.T.;
RA "Computational searching and mutagenesis suggest a structure for the
RA pentameric transmembrane domain of phospholamban."
RL Nat. Struct. Biol. 2:154-162(1995).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=98170970; PubMed=9512019;
RA Herzyk P., Hubbard R.E.;
RT "Using experimental information to produce a model of the
RT transmembrane domain of the ion channel phospholamban."
RL Biophys. J. 74:1203-1214(1998).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M63603; AAA60083.1; -
DR EMBL: M60411; AAA60109.1; -
DR EMBL: AF177764; AAD55950.1; -
DR EMBL: BC005269; AAH05269.1; -
DR PIR: A40424; A40424.
DR PDB: 1K9N; Model: A/B/C/D/E=35-52.
DR PDB: 1KCH; Model: A/B/C/D/E=35-52.
DR PDB: 1PIN; Model: A/B/C/D/E=35-52.
DR PDB: 1PLP; Model: @=1-25.
DR PDB: 1PSL; Model: A/B/C/D/E=1-52.
DR Genew: HGNC:9080; PLN.
DR H-InvDB: HIX0006177; -.
DR MIM: 172405; -.
DR InterPro: IPR005984; P_lamban.
DR Pfam: PF04272; Phospholamban; 1.
DR TIGRFAMs: TIGRF001665; PLB; 1.
DR TIGRFAMs: TIGR01294; P_lamban; 1.
KW 3D-structure; Acetylation; Phosphorylation; Transmembrane.
FT DOMAIN 1 31 Cytoplasmic (Potential).
FT TRANSMEM 32 52 Potential.
FT MOD_RES 1 1 N-acetylmethionine (By similarity).
FT MOD_RES 16 16 Phosphoserine (by PKA) (By similarity).
FT MOD_RES 17 17 Phosphothreonine (by CamK) (By
FT similarity).
FT TURN 2 3
FT HELIX 4 14
FT TURN 15 15
SQ SEQUENCE 52 AA; 6108 MW; 0766304A76A854D3 CRC64;
Query Match 96.0%; Score 144; DB 1; Length 52;
Best Local Similarity 96.7%; Pred. No. 6,3e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QARQNLQNLFINFCILICLLICITIVML 30
DB 23 QARQNLQNLFINFCILICLLICITIVML 52

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RESULT 7
ID PPLA_CHICK STANDARD; PRT; 52 AA.
AC P26677;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name=PLB;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91170195; PubMed=1825996;
RA Toyofuku T., Zak R.;
RT "Characterization of cDNA and genomic sequences encoding a chicken
RT phospholamban."
RL J. Biol. Chem. 266:5375-5383(1991).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M59039; AAA62738.1; -
DR EMBL: M59037; -; NOT_ANNOTATED_CDS.
DR EMBL: M59038; AAA63167.1; -
DR PIR: A39535; A39535.
DR HSSP: P07473; 1RJK.
DR InterPro: IPR005984; P_lamban.
DR Pfam: PF04272; Phospholamban; 1.
DR TIGRFAMs: TIGR01294; P_lamban; 1.
DR TIGRFAMs: TIGR01294; P_lamban; 1.
KW Acetylation; Phosphorylation; Transmembrane.
FT DOMAIN 1 31 Cytoplasmic (Potential).
FT TRANSMEM 32 52 Potential.
FT MOD_RES 1 1 N-acetylmethionine (By similarity).
FT MOD_RES 16 16 Phosphoserine (by PKA) (By similarity).
FT MOD_RES 17 17 Phosphothreonine (by CamK) (By
FT similarity).
SQ SEQUENCE 52 AA; 6091 MW; F95F86C36A0C4D3B CRC64;
Query Match 91.3%; Score 137; DB 1; Length 52;
Best Local Similarity 90.0%; Pred. No. 4,3e-09;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QARQNLQNLFINFCILICLLICITIVML 30
DB 23 QARQNLQNLFINFCILICLLICITIVML 52
RESULT 8
ID 081216 PRELIMINARY; PRT; 792 AA.
AC 081216;
DT 01-MAR-2003 (TRENDBLrel. 23, Created)
DT 01-MAR-2003 (TRENDBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENDBLrel. 23, Last annotation update)

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RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U00067; AKK20074.1; -.
DR PIR; T34299; T34299.
DR WormBase; WBGene0001828; F54E7.5.
DR WormPep; F54E7.5; CE01316.
KW Hypothetical protein.
SQ
SEQUENCE 305 AA; 34300 MW; 0090B96DF621228 CRC64;

Query Match
Best Local Similarity 39.0%; Score 58.5; DB 2; Length 305;
Matches 13; Conservativity 54.2%; Pred. No. 32;
Mismatches 3; Indels 7; Gaps 1;

QY 7 ONLFNFCILICILICIIYML 30
      :| | | | | | | | | |
DB 186 QHLI-ACILICLTFEIIVF 208

RESULT 10
SARL_MOUSE
SARL_MOUSE STANDARD; PRT; 31 AA.
AC 09COD6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sarcoplasm.
CN Name=lin;
OS Mus musculus (Mouse).

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 XM NCB1_TaxID=10090;
 OX [1]
 RN [1] Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

RC STEINLE=C57BL/6J; TISSUE=Stomach, and Tongue;
RX MELLINE=22354683; Pubmed=12466851; doi=10.1038/nature01266;
RA Okazaki Y., Furuta M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Idarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA GRIMMOND S., HIROKAWA N., JACKSON L.O., PALVIS E.O.,
RA KANAI A., KAWAJI H., KAWASAWA Y., KEDZIERSKI R.M., KING B.L.,
RA

RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A., MacIott D.R., Maltais I., Marchionni I., McKenzie I., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Potrowsky N., Pillat P., Pontius T. II, Qi D., Ramachandran S.

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
KA Shitaki T., Waki K., Kawai J., Aizawa K., Akakawa I., Fukuda S.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston P., Iander E. S., Rogers J.

RA Birney E., Hayashizaki Y.;

RT 60,770 full-length cDNAs.";

RN [2]

RC TISSUE=Mammary gland;
KF SEQUENCE FROM N:A;
KF

RA Strausberg R L, Feinold E A, Grouse J, H. Derge J. G. J.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603895;

RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
PA	Alteschul S F, Zeeberg B, Bueto C H, Schaefer C E, Bhat N.K.

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.T., Ueda T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Locantello N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBUNIT: Associated with calcium ATPase SERCA1.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Sarcoplasmic reticulum.
 CC -----
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 CC -----
 CC EMBL; AK008863; -; NOT ANNOTATED_CDS.
 CC -----
 DR EMBL; AK008896; BAB25959.1; -;
 DR EMBL; AK009005; BAB26019.1; -;
 DR EMBL; AK009809; BAB26516.1; -;
 DR EMBL; BC028496; AAH28496.1; -;
 DR HSSP; 000631; 1JDM.
 DR MGD; MGI:191652; Sln.
 DR InterPro; IPR008028; Sarcoplipin.
 DR Pfam; PF05366; Sarcoplipin; 1.
 DR Sarcoplasmic reticulum; Transmembrane.
 FT TRASNMEM 8 25 Potential.
 FT SEQUENCE 31 AA; 3808 MW; 9B310161575EF81D CRC64;
 SQ

Query Match 38.7%; Score 58; DB 1; Length 31;
 Best Local Similarity 45.8%; Pred. No. 6.3;
 Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

4 ONLQNLFTNFCILICILICITIV 27
 Db 3 RSTQELFNFTVLTIVLIMLV 26

RESULT 11

06SL67 PRELIMINARY; PRT; 31 AA.
 AC 06SL67;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Sarcoplipin.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Histar; TISSUE=Arrium;
 RA Minamideba S., Yokoyama U., Sato Y., Nakagome M., Mouri M., Uemura N.,
 RA Horii H., Ishikawa Y.,
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY456000; AAR19044.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030234; P:enzyme regulator activity; IEA.
 DR InterPro; IPR008028; Sarcoplipin.
 DR Pfam; PF05366; Sarcoplipin; 1.
 DR SEQUENCE 31 AA; 3808 MW; 9B310161575EF81D CRC64;
 SQ

Query Match 38.7%; Score 58; DB 2; Length 31;
 Best Local Similarity 45.8%; Pred. No. 6.3;
 Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

4 ONLQNLFTNFCILICILICITIV 27
 Db 3 RSTQELFNFTVLTIVLIMLV 26

RESULT 12

070V94 PRELIMINARY; PRT; 130 AA.
 AC 070V94;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 1 (fragment).
 GN Name=NADH1;
 OS Cotesia kazak.
 OG Microchordon.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoidea;
 OC Braconidae; Microgasterinae; Cotesia.
 OX NCBI_TaxID=217438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Michel-Salzat A., Whitfield J.B.;
 RT "Preliminary evolutionary relationships within the parasitoid wasp
 RT genus Cotesia (Hymenoptera: Braconidae: Microgasterinae): combined
 RT analysis of four molecular markers.";
 RL Syst. Entomol. 29:371-382(2004).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- SIMILARITY: Belongs to the complex I subunit 1 family.
 CC EMBL; AJ535986; CAD59806.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR01694; Resp_NADH_dhl.
 DR Pfam; PF00146; NADHdh; 1.
 DR Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
 FT NON_TER 1 130
 FT NON_TER 1 130
 FT SEQUENCE 130 AA; 15080 MW; 134A6A937BB37DF5 CRC64;
 SQ

Query Match 38.3%; Score 57.5; DB 2; Length 130;
 Best Local Similarity 53.3%; Pred. No. 22;
 Matches 16; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

5 NLQNL-----PINFCILICILICITIV 29
 Db 96 NLVNLNFKFTNFSMTYPLMLITISML 125

RESULT 13

09PIM9 PRELIMINARY; PRT; 169 AA.
 AC 09PIM9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedLocusNames=Cj0266.3, Cj0266c;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
 RA Parthill J., Wren B.W., Mungall K.L., Kettley J.M., Churche C.M.,
 RA Basham D., Chillingworth T., Davies R.M., Felwell T., Holroyd S.,

RA Jagele K., Kariyhev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrrell B.G.;
 RT "The genome sequence of the food-borne pathogen *Campylobacter jejuni*
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 DR EMBL; AL139074; CAB2734.1; -.
 DR PIR; A81445; A81445.
 DR InterPro; IPR010916; TONB_Box_N.
 DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 169 AA; 19512 MW; E3ZDF1293031871B CRC64;
 Query Match 38.0%; Score 57; DB 2; Length 169;
 Best Local Similarity 52.6%; Pred. No. 30;
 Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Oy 11 INPCLILICLLICITVML 29
 Db 9 IAFILILICPALICILIFL 27
 RESULT 14
 Q6V2B7 PRELIMINARY; PRT; 35 AA.
 AC Q6V2B7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 OS Bidesodes limestonensis.
 CC Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Coleoptera; Adephaga; Dytiscidae;
 CC Hydrophorinae; Bidesmini; Bidesodes.
 CC NCBI_TaxID=245104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14761060;
 RA Lays R., Watts C.H.S., Cooper S.J.B., Humphreys W.F.;
 RT "Evolution of subterranean diving beetles (Coleoptera: Dytiscidae:
 RT Hydrophilini, Bidesmini) in the arid zone of Australia.";
 RL Evolution 57:2819-2834(2003).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- SIMILARITY: Belongs to the complex I subunit 1 family.
 DR EMBL; AY338827; AAR0201.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR InterPro; IPR001694; Resp_NADH_dhl.
 DR Pfam; PF00146; NADHdh; 1.
 KM Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
 FT NON TER 35
 SQ SEQUENCE 35 AA; 4126 MW; 4FBPF64DC8B6F20 CRC64;
 Query Match 37.3%; Score 56; DB 2; Length 35;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 12; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
 Oy 10 FINPCLILICLLICITV 27
 Db 4 FYDFMLILICLLIVICLV 23
 RESULT 15
 Q8BS41 PRELIMINARY; PRT; 110 AA.
 AC Q8BS41;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
 DE mescutis library, clone:R530008A08 product:hypothetical protein, full
 DE insert sequence.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA The FANTOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=204993704; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subfraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.153600;
 RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwaigi K.,
 RA Fujiwaka E., Inoue K., Togawa Y., Izawa M., Ohara E., Watanaki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka K., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kohjima Y., Kondo S., Kono H., Koda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK040657; BAC30658.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 110 AA; 12777 MW; C6D74D054430317B CRC64;
 Query Match 37.3%; Score 56; DB 2; Length 110;
 Best Local Similarity 42.9%; Pred. No. 29;
 Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
 Oy 10 FINPCLILICLLICITVML 30
 | : | : | : | : | : |

Db 86 PALCFVLFVLFCLIAKFL 106

Search completed: July 7, 2005, 15:41:08
Job time : 395 secs

This Does Rink (uspto)

APPLICANT: Lotta, Timo

;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; CURRENT FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; EARLIER FILING DATE: 1997-09-24
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Oryctolagus cuniculus
US-09-252-063-4

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARONLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARONLQNLFINFCLILICLLILICIIYVWL 52

RESULT 3
US-09-252-063-5
;; Sequence 5, Application US/09252063
;; Patent No. 6538022
;; GENERAL INFORMATION:
;; APPLICANT: Pollesello, Piero
;; APPLICANT: Ovasaka, Martti
;; APPLICANT: Tenhunen, Jukka
;; APPLICANT: Viidgren, Jukka
;; APPLICANT: Viipertula-Ikonen, Marjo
;; APPLICANT: Tilgmann, Carola
;; APPLICANT: Lotte, Timo
;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; CURRENT FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; EARLIER FILING DATE: 1997-09-24
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Rattus sp.
US-09-252-063-5

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARONLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARONLQNLFINFCLILICLLILICIIYVWL 52

RESULT 4
US-09-252-063-6
;; Sequence 6, Application US/09252063
;; Patent No. 6538022
;; GENERAL INFORMATION:
;; APPLICANT: Pollesello, Piero
;; APPLICANT: Ovasaka, Martti
;; APPLICANT: Tenhunen, Jukka
;; APPLICANT: Viidgren, Jukka
;; APPLICANT: Viipertula-Ikonen, Marjo
;; APPLICANT: Tilgmann, Carola
;; APPLICANT: Lotte, Timo

;; APPLICANT: Kaivola, Juha
;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; CURRENT FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; EARLIER FILING DATE: 1997-09-24
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-09-252-063-6

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARONLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARONLQNLFINFCLILICLLILICIIYVWL 52

RESULT 5
US-09-549-872B-14
;; Sequence 14, Application US/09549872B
;; Patent No. 6540996
;; GENERAL INFORMATION:
;; APPLICANT: Zwaal, Richard
;; APPLICANT: Groenen, Jose
;; APPLICANT: Bogaert, Thierry
;; TITLE OF INVENTION: COMPOUND SCREENING METHODS
;; FILE REFERENCE: D00590/70008 (JRV/RE)
;; CURRENT APPLICATION NUMBER: US/09/549,872B
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: GB 9908670.4
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: US 60/129,596
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: GB 9912736.7
;; PRIOR FILING DATE: 1999-06-01
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Sus sp.
US-09-549-872B-14

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARONLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARONLQNLFINFCLILICLLILICIIYVWL 52

RESULT 6
US-09-549-872B-15
;; Sequence 15, Application US/09549872B
;; Patent No. 6540996
;; GENERAL INFORMATION:
;; APPLICANT: Zwaal, Richard
;; APPLICANT: Groenen, Jose
;; APPLICANT: Bogaert, Thierry
;; TITLE OF INVENTION: COMPOUND SCREENING METHODS
;; FILE REFERENCE: D00590/70008 (JRV/RE)
;; CURRENT APPLICATION NUMBER: US/09/549,872B
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: GB 9908670.4

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; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-872B-15
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Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  QARONLQNLFINFCILICLLICLLIIVMLL 30
Db      23  QARONLQNLFINFCILICLLICLLIIVMLL 52
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```

RESULT 7
US-09-722-440-3
; Sequence 3, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis sp.
US-09-722-440-3
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Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  QARONLQNLFINFCILICLLICLLIIVMLL 30
Db      23  QARONLQNLFINFCILICLLICLLIIVMLL 52
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RESULT 8
US-09-722-440-4
; Sequence 4, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; APPLICANT: Kaivola, Juh
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
```

```

; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-722-440-4
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Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  QARONLQNLFINFCILICLLICLLIIVMLL 30
Db      23  QARONLQNLFINFCILICLLICLLIIVMLL 52
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RESULT 9
US-09-722-440-5
; Sequence 5, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-722-440-5
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Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1  QARONLQNLFINFCILICLLICLLIIVMLL 30
Db      23  QARONLQNLFINFCILICLLICLLIIVMLL 52
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RESULT 10
US-09-722-440-6
; Sequence 6, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; APPLICANT: Kaivola, Juh
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
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; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-722-440-6

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

Qy 1 QARQNLQNLFFNFCILICLLICILICIIWML 30
Db 23 QARQNLQNLFFNFCILICLLICILICIIWML 52

RESULT 11
US-09-252-063-1
; Sequence 1, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; PRIOR FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-063-1

Query Match 96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARQNLQNLFFNFCILICLLICILICIIWML 30
Db 23 QARQNLQNLFFNFCILICLLICILICIIWML 52

RESULT 12
US-09-252-063-2
; Sequence 2, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo

; APPLICANT: Kaivoja, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; PRIOR FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-252-063-2

Query Match 96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARQNLQNLFFNFCILICLLICILICIIWML 30
Db 23 QARQNLQNLFFNFCILICLLICILICIIWML 52

RESULT 13
US-09-722-440-1
; Sequence 1, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-722-440-1

Query Match 96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARQNLQNLFFNFCILICLLICILICIIWML 30
Db 23 QARQNLQNLFFNFCILICLLICILICIIWML 52

RESULT 14
US-09-722-440-2
; Sequence 2, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola


```

; APPLICANT: Lotte, Timo
; APPLICANT: Kalvola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-722-440-2

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```

Query Match          96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 QARQNLQNLFINFCILICLILICLIIVML 30
Db      23 QARQNLQNLFINFCILICLILICLIIVML 52

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RESULT 15

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US-09-949-016-7310
; Sequence 7310, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7310
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7310

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Query Match          96.0%; Score 144; DB 4; Length 89;
Best Local Similarity 96.7%; Pred. No. 4.8e-12;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      60 QARQNLQNLFINFCILICLILICLIIVML 89

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Search completed: July 7, 2005, 15:44:07
Job time : 91 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2005, 15:41:16 ; Search time 386 Seconds
(without alignments)
30.026 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150
Sequence: 1 QARQNLQNLFINFCLILICLLICILIVML 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	150	100.0	52	9	US-09-954-571-4
4	150	100.0	52	9	US-09-954-571-5
5	150	100.0	52	14	US-10-371-101-14
6	150	100.0	52	14	US-10-371-101-15
7	150	100.0	53	16	US-10-760-721-1
8	144	96.0	52	9	US-09-954-571-1
9	144	96.0	52	9	US-09-954-571-2
10	144	96.0	52	16	US-10-408-765A-478
11	144	96.0	52	16	US-10-705-791-1

12	144	96.0	52	16	US-10-705-791-3	Sequence 3, Appl1
13	144	96.0	52	16	US-10-705-791-4	Sequence 4, Appl1
14	144	96.0	52	16	US-10-705-791-5	Sequence 5, Appl1
15	144	96.0	52	16	US-10-705-791-6	Sequence 6, Appl1
16	144	96.0	79	16	US-10-705-791-17	Sequence 17, Appl1
17	144	96.0	79	16	US-10-705-791-18	Sequence 18, Appl1
18	140	93.3	52	16	US-10-705-791-2	Sequence 2, Appl1
19	140	93.3	79	16	US-10-705-791-19	Sequence 19, Appl1
20	137	91.3	30	16	US-10-724-532-2	Sequence 2, Appl1
21	130	86.7	27	16	US-10-815-514-7	Sequence 7, Appl1
22	130	86.7	27	16	US-10-877-930-7	Sequence 7, Appl1
23	130	86.7	27	16	US-10-877-930-7	Sequence 7, Appl1
24	130	86.7	90	16	US-10-815-514-25	Sequence 25, Appl1
25	130	86.7	90	16	US-10-877-930-25	Sequence 25, Appl1
26	130	86.7	90	17	US-10-873-594-25	Sequence 25, Appl1
27	86	57.3	53	16	US-10-760-721-4	Sequence 4, Appl1
28	76	50.7	53	16	US-10-760-721-2	Sequence 2, Appl1
29	76	50.7	53	16	US-10-760-721-3	Sequence 3, Appl1
30	75	50.0	16	10	US-09-255-658-19	Sequence 19, Appl1
31	75	50.0	16	10	US-09-491-614-18	Sequence 18, Appl1
32	75	50.0	16	14	US-10-161-205-17	Sequence 17, Appl1
33	75	50.0	16	14	US-10-101-001-17	Sequence 17, Appl1
34	62	41.3	27	16	US-10-760-721-6	Sequence 6, Appl1
35	58	38.7	27	16	US-10-760-721-5	Sequence 5, Appl1
36	57	37.3	137	16	US-10-767-701-42239	Sequence 42239, A
37	56	37.3	297	15	US-10-282-122A-73638	Sequence 73638, A
38	55.5	37.0	400	10	US-09-769-736-34	Sequence 34, Appl1
39	55	36.7	31	16	US-10-723-860-3853	Sequence 3853, Ap
40	55	36.7	173	16	US-10-437-963-175427	Sequence 175427, A
41	55	36.7	230	15	US-10-104-067-3554	Sequence 3554, Ap
42	55	36.7	394	15	US-10-282-122A-45727	Sequence 45727, A
43	55	36.7	579	17	US-10-495-148-43	Sequence 43, Appl1
44	55	36.7	651	17	US-10-495-148-47	Sequence 47, Appl1
45	55	36.7	669	10	US-09-790-852-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-10-724-532-1
; Sequence 1, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarcoplasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-724-532-1

Query Match 100.0%; Score 150; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 QARQNLQNLFINFCLILICLLICILIVML 30

RESULT 2
US-09-954-571-3
; Sequence 3, Application US/09954571
; Publication No. US20020032167A1

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 52
TYPE: PRT
ORGANISM: Canis familiaris
US-09-954-571-3

Query Match 100.0%; Score 150; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 QARONLQNLFINFCLILICLLICIIIVML 52

RESULT 3
US-09-954-571-4
Sequence 4, Application US/09954571
Publication No. US20020032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 52
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-571-4

Query Match 100.0%; Score 150; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 QARONLQNLFINFCLILICLLICIIIVML 52

RESULT 4
US-09-954-571-5
Sequence 5, Application US/09954571
Publication No. US20020032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 52
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-954-571-5

Query Match 100.0%; Score 150; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 QARONLQNLFINFCLILICLLICIIIVML 52

RESULT 5
US-10-371-101-14
Sequence 14, Application US/10371101
Publication No. US2003014995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590,70035, US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 52
TYPE: PRT
ORGANISM: Sus sp.
US-10-371-101-14

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Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 QARONLQNLFINFCLILICLLICIIIVML 52

RESULT 6
US-10-371-101-15
Sequence 15, Application US/10371101
Publication No. US2003014995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590,70035, US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7

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; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-101-15

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Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 23 QARONLQNLFINFCLILICLLICITIVMLL 52

RESULT 7
US-10-760-721-1
; Sequence 1, Application US/10760721
; Publication No. US20040213400A1
; GENERAL INFORMATION:
; APPLICANT: Slovlic, Avram M.
; APPLICANT: Summa, Christopher M.
; APPLICANT: Saven, Jeffrey G.
; APPLICANT: Degrado, William F.
; APPLICANT: Kono, Hidetoshi
; TITLE OF INVENTION: Computational Design of a Water-Soluble Analog of a Protein, such
; FILE REFERENCE: 1694.0540001
; CURRENT APPLICATION NUMBER: US/10/760,721
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Canine PUS
US-10-760-721-1

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Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 QARONLQNLFINFCLILICLLICITIVMLL 53

RESULT 8
US-09-954-571-1
; Sequence 1, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R.
; APPLICANT: Hoshijima, Maehiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: Mutant form of human protein sequence
US-09-954-571-1

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Best Local Similarity 96.7%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 23 QARONLQNLFINFCLILICLLICITIVMLL 52

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US-09-954-571-2
; Sequence 2, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R.
; APPLICANT: Hoshijima, Maehiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-571-2

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Best Local Similarity 96.7%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QARONLQNLFINFCLILICLLICITIVMLL 30
DB 23 QARONLQNLFINFCLILICLLICITIVMLL 52

RESULT 10
US-10-408-765A-478
; Sequence 478, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale B.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-478

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Best Local Similarity 96.7%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-5

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Best Local Similarity 96.7%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

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Db 23 QAROKLQNLFINFCILICILICILICIVML 52

RESULT 15
US-10-705-791-6
Sequence 6, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Huaping
APPLICANT: Hoshijima, Masahiko
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yabin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-6

Query Match 96.0%; Score 144; DB 16; Length 52;
Best Local Similarity 96.7%; Pred. No. 2e-10; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARONLQNLFINFCILICILICILICIVML 30
Db 23 QAROKLQNLFINFCILICILICILICIVML 52

Search completed: July 7, 2005, 16:12:48
Job time : 386 secs

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Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Qy 21 LeuLeuIleCysIleIleValMetLeuLeu 30

Db 127 TTGCTGATTTCATCATCTGATGCTTC 156

RESULT 2

BD247911 159 bp DNA linear PAT 17-JUN-2003
LOCUS Method for screening compounds.
DEFINITION BD247911
ACCESSION BD247911 GI:33057681
VERSION JP 2002541859-A/13.
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV

COMMENT

OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG PLB cDNA FH
Key Location/Qualifiers
FT source 1..159
/organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-724-532-1 (1-30) x BD247911 (1-159)

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Db 67 CAGGACGCTCAAAACCTTCAGAACCTATTTCATTTCTGTCTCATCTTAATATGCTTC 126

Qy 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 127 TTGCTGATTTCATCATCTGATGCTTC 156

RESULT 3

AR302003 159 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 9 from patent US 6540996.
DEFINITION AR302003
ACCESSION AR302003
VERSION AR302003.1 GI:31689908
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 9 01-APR-2003;
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-724-532-1 (1-30) x AR302003 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20

Db 67 CAGGACGCTCAAAACCTTCAGAACCTATTTCATTTCTGTCTCATCTTAATATGCTTC 126

Qy 21 LeuLeuIleCysIleIleValMetLeuLeu 30

Db 127 TTGCTGATTTCATCATCTGATGCTTC 156

RESULT 4

AR302007 159 bp DNA linear PAT 12-JUN-2003
LOCUS AR302007
DEFINITION Sequence 13 from patent US 6540996.
ACCESSION AR302007
VERSION AR302007.1 GI:31689912
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 13 01-APR-2003;
FEATURES Location/Qualifiers
source 1..159
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-724-532-1 (1-30) x AR302007 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20

DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCGTCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 TTGCTGATTGGCATCATCGTGAATGCTTCTC 156

RESULT 5
AX040487 159 bp DNA linear PART 18-NOV-2000
DEFINITION Sequence 9 from Patent WO0063426.
ACCESSION AX040487
VERSION AX040487.1 GI:11230276
KEYWORDS
SOURCE
ORGANISM Sus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 9 26-OCT-2000;
DEVGEN NV (BE)
FEATURES
source location/Qualifiers
1..159
/organism="Sus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:9826"

ORIGIN
Alignment Scores:
Pred. No.: 1,11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-724-532-1 (1-30) x AX040487 (1-159)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCGTCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 TTGCTGATTGGCATCATCGTGAATGCTTCTC 156

RESULT 6
AX040491 159 bp DNA linear PART 18-NOV-2000
DEFINITION Sequence 13 from Patent WO0063426.
ACCESSION AX040491
VERSION AX040491.1 GI:11230280
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 13 26-OCT-2000;
DEVGEN NV (BE)
FEATURES
source location/Qualifiers
1..159
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HUMANIZED PIG PLB CDNA"

ORIGIN
Alignment Scores:
Pred. No.: 1,11e-09 Length: 159

Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-724-532-1 (1-30) x AX040491 (1-159)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCGTCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 TTGCTGATTGGCATCATCGTGAATGCTTCTC 156

RESULT 7
S95853 159 bp mRNA linear ROD 07-MAY-1993
LOCUS phospholamban [rats, aortic smooth muscle, mRNA, 159 nt].
DEFINITION S95853
ACCESSION S95853
VERSION S95853.1 GI:247932
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 159)
AUTHORS Hwang, K.S. and Nadal-Ginard, B.
TITLE Cloning phospholamban cDNA from rat aortic smooth muscle
JOURNAL Adv. Exp. Med. Biol. 304, 387-395 (1991)
MEDLINE 92206263
PUBMED 1725098
REMARK Genbank staff at the National Library of Medicine created this entry (NCBI glibseq 95853) from the original journal article.

FEATURES
source location/Qualifiers
1..159
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
1..159
/gene="phospholamban, PLN"
1..159
/gene="phospholamban, PLN"
/note="PLN"
/codon_start=1
/product="phospholamban"
/protein_id="AAB21903.1"
/db_xref="GI:247933"
/translation="MEKVQYLRSAIRASSTIEMPOQARQNLQNLFINFCLLICLL
ICIIYML"

ORIGIN
Alignment Scores:
Pred. No.: 1,11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-724-532-1 (1-30) x S95853 (1-159)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCGTCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 CTGCTGATCTGCATCATTTGTGATGCTCTCG 156

RESULT 8

AY514751
LOCUS AY514751 314 bp DNA linear MAM 02-JUL-2004
DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
ACCESSION AY514751
VERSION AY514751.1 GI:48476898
KEYWORDS
SOURCE
ORGANISM Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE
1 (bases 1 to 314)
Housley,D.J.E., Ritzert,E. and Venta,P.J.
Comparative radiation hybrid map of canine chromosome 1
incorporating SNP and indel polymorphisms
Genomics 84 (2), 248-264 (2004)
2 (bases 1 to 314)
Housley,D.J.E., Ritzert,E. and Venta,P.J.
Direct Submission
Submitted (29-DEC-2003) Small Animal Clinical Sciences and
Microbiology and Molecular Genetics, Michigan State University,
College of Veterinary Medicine, East Lansing, MI 48824-1314, USA

FEATURES
source
location/Qualifiers
1..314
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/note="sequence information was obtained from a pool of
ten breeds: German shepherd dog; Beagle; German shorthair
pointer; Scottish terrier; Doberman pinscher; Greyhound;
Siberian husky; Labrador retriever; Collie; Cocker
spaniel; additional sequence was obtained from a single
mixed breed dog of unknown origin"
<1..>314
/gene="PLN"
<1..>314
/gene="PLN"
/number=2
1..39
/gene="PLN"
<40..>198
/gene="PLN"
/product="phospholamban"
40..198
/gene="PLN"
/codon_start=1
/product="phospholamban"
/protein_id="AA04582.1"
/db_xref="GI:48476898"
/translation="MDKYQYLRSAIRASTIEMPOARQNLQNLFINFCILICLL
ICILVML"
199..>314
/gene="PLN"

ORIGIN
3' UTR

Alignment Scores:
Pred. No.: 2,11e-09 Length: 314
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x AY514751 (1-314)

QY 1 GlnAaAAGGAnAnLeuGlnAnLeuPheIleAnPheCysLeuIleLeuIleCysLeu 20
Db 106 CAAGCAGCTCAGAACTCTCAAGAACCTATTATTAATTTCTGCTCATTTATATATGCTC 165

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 166 TTGTTGATCTGATCATTTGTATGCTTCTC 195

RESULT 9

S95849
LOCUS S95849 386 bp mRNA linear ROD 16-DEC-2002
DEFINITION Rattus sp. phospholamban (Pln) mRNA, complete cds.
ACCESSION S95849
VERSION S95849.1 GI:247934
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 386)
Hwang,K.S. and Nadal-Ginard,B.
Cloning phospholamban cDNA from rat aortic smooth muscle
Adv. Exp. Med. Biol. 304, 387-395 (1991)
JOURNAL MEDLINE 92206263
PUBMED 1725098

REMARK GenBank staff at the National Library of Medicine created this
entry (NCBI gi247934) from the original journal article.
This sequence comes from Fig. 2.

FEATURES
source
location/Qualifiers
1..386
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/tissue_type="cardiac smooth muscle"
1..386
/gene="Pln"
159..317
/gene="PLN"
/codon_start=1
/product="phospholamban"
/protein_id="P0AN6727.1"
/db_xref="GI:26986719"
/translation="MEKYQYLRSAIRASTIEMPOARQNLQNLFINFCILICLL
ICILVML"

ORIGIN

Alignment Scores:
Pred. No.: 2,56e-09 Length: 386
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x S95849 (1-386)

QY 1 GlnAaAAGGAnAnLeuGlnAnLeuPheIleAnPheCysLeuIleLeuIleCysLeu 20
Db 225 CAAGCAGCTCAGAACTCTCAAGAACCTATTATTAATTTCTGCTCATTTATATATGCTG 284

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 285 CTGCTGATCTGATCATTTGTATGCTTCTG 314

RESULT 10
BC061097 648 bp mRNA linear ROD 30-JUN-2004
LOCUS BC061097
DEFINITION Mus musculus phospholamban, mRNA (cDNA clone MGC:74215
IMAGE:6772294), complete cds.
ACCESSION BC061097
VERSION BC061097.1 GI:38173946
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
1 (bases 1 to 648)
Straubeberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shermen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diachenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stappleton, M., Soares, M. B., Bonaldo, M. P., Casavant, T. L., Scherdt, T. E., Brownstein, M. J., Uedlin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Kana, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Malley, S. J., Bosak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunatane, P. H., Richard, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shvachenko, Y., Bouffard, G. G., Blakeley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butlerfield, Y. S., Krzywinski, M. I., Skliska, V., Smallos, D. E., Scherch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 648)
Strausberg, R.
Direct Submission
Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein / Ted Uedlin
Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mdc@axil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAL Plate: 53 Row: 9 Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963502.

FEATURES
source
location/Qualifiers
1..648
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MGC:74215 IMAGE:6772294"
/issue_type="Testis, mouse"
/clone_lib="NIH_MGC_169"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
1..648
/gene="pin"
/note="synonym: PUB"
/db_xref="LocustID:18821"
/db_xref="MGI:97622"
211..369
/gene="pin"
/codon_start=1
/product="phospholamban"
/protein_id="AAH61097.1"
/db_xref="GI:38173947"
/db_xref="LocustID:18821"
/db_xref="MGI:97622"
/translation="MEKVOYLRSARASTIEMPOQARONLQNFIFNCLILCLL
ICIIIVML"

ORIGIN
Alignment Scores:
Pred. No.: 4.17e-09 Length: 648

Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x BC061097 (1-648)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
277 CAGGACGGCGAAATCTCGAAGACCATTTATCAATTTCTGCTCATTTGATGCTCG 336

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
337 CTGCTGATCTGCATCTGATGCTGCTG 366

RESULT 11
RNPFLAMB 701 bp mRNA linear ROD 09-JUL-1993
LOCUS RNPFLAMB
DEFINITION R.norvegicus mRNA for phospholamban.
ACCESSION X71068
VERSION X71068.1 GI:313809
KEYWORDS phospholamban.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS 1
TITLE Shanahan, C.M., Weissberg, P.L. and Metcalfe, J.C.
JOURNAL Isolation of gene markers of differentiated and proliferating
MEDLINE vascular smooth muscle cells
PUBMED Circ. Res. 73 (1), 193-204 (1993)
8508530

2 (bases 1 to 701)
Shanahan, C.M.
Direct Submission
Submitted (26-FEB-1993) C.M. Shanahan, University of Cambridge,
Dept of Biochemistry, Tennis Court Road, Cambridge CB2 1QM, UK

FEATURES
source
location/Qualifiers
1..701
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/clone="2RB7"
/issue_type="aorta smooth muscle"
/clone_lib="lambda-Zap"
/dev_stage="adult"
174..332
/codon_start=1
/product="phospholamban"
/protein_id="CAA50394.1"
/db_xref="GI:313810"
/db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVOYLRSARASTIEMPOQARONLQNFIFNCLILCLL
ICIIIVML"

CDS
ORIGIN
Alignment Scores:
Pred. No.: 4.49e-09 Length: 701
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x RNPFLAMB (1-701)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
|||||

Db 240 CAAGCGCTCAGAACCTCCAGAACCTCTTTATCAATTCTGTCTCATCTGATATGCTG 299

Qy 21 LeuLeuileCysIleIleValMetLeuLeu 30
|||||
Db 300 CTGCTGATATGCATCATCTGTATGCTTCTG 329

RESULT 12

SSPUB 737 bp mRNA linear MAM 12-SEP-1993

LOCUS Pig mRNA for phospholamban.

DEFINITION X15075

ACCESSION X15075.1 GI:2055

VERSION calcium regulatory protein; phospholamban; transmembrane protein.

KEYWORDS Sus scrofa (pig)

SOURCE Sus scrofa

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 737)

AUTHORS Misiak, H., Whyte, F., Eggermont, J.A., De Jaegere, S., Verdoomen, H., Raeymaekers, L., and Casteele, R.

TITLE cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle

JOURNAL Biochem. J. 262 (1), 353-356 (1989)

MEDLINE 90056437

PUBMED 2530978

REFERENCE 2 (bases 1 to 737)

AUTHORS Eggermont, J.A.

TITLE Direct Submission

JOURNAL Submitted (13-APR-1989) Eggermont J.A., Laboratorium Voor Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49, B-3000 Leuven, Belgium

COMMENT See <Y00399> for canine phospholamban and <Y00761> for rabbit phospholamban.

FEATURES

source Data kindly reviewed (12-OCT-1989) by Eggermont J. A.

location/Qualifiers

1. 737

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="PLB 7"

/tissue_type="smooth muscle"

/clone_lib="lambda gtl1"

/dev_stage="2-day-old piglet"

173..331

/note="unmated protein product; phospholamban (AA 1-52)"

/codon_start=1

/protein_id="CA33171.1"

/db_xref="GI:2056"

/db_xref="GOL:P07473"

/db_xref="UniProt/Swiss-Prot:P07473"

/translation="MDKVQYLTRSAIRASTIEMPOQARQNLQNLFINFCLILCLL ICIIVML"

716..721

/note="pot. polyA signal"

737

/note="polyA site"

ORIGIN

Alignment Scores:

Pred. No.: 4.71e-09 Length: 737

Score: 150.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

US-10-724-532-1 (1-30) x SSPUB (1-737)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
|||||
Db 239 CAACGACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCATCTTATATGCTC 298

Qy 21 LeuLeuileCysIleIleValMetLeuLeu 30

Db 299 TTGCTGATTTGCATCATCTGATGCTTCTC 328

RESULT 13

DOGPHL 832 bp mRNA linear MAM 27-APR-1993

LOCUS Canine cardiac phospholamban mRNA.

DEFINITION M16012

ACCESSION M16012.1 GI:164043

VERSION phospholamban.

KEYWORDS Canis lupus (gray wolf)

SOURCE Canis lupus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 832)

AUTHORS Fujii, J., Ueno, A., Kitano, K., Tanaka, S., Kadoya, M., and Tada, M.

TITLE Complete complementary DNA-derived amino acid sequence of canine cardiac phospholamban

JOURNAL J. Clin. Invest. 79 (1), 301-304 (1987)

MEDLINE 87083954

PUBMED 3793929

COMMENT Original

FEATURES

source text: Dog cDNA to mRNA.

location/Qualifiers

1. 832

/organism="Canis lupus"

/mol_type="mRNA"

/db_xref="taxon:9612"

181..339

/note="cardiac phospholamban"

/codon_start=1

/protein_id="AAA30884.1"

/db_xref="GI:164044"

/translation="MDKVQYLTRSAIRASTIEMPOQARQNLQNLFINFCLILCLL ICIIVML"

ORIGIN

Alignment Scores:

Pred. No.: 5.28e-09 Length: 832

Score: 150.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

US-10-724-532-1 (1-30) x DOGPHL (1-832)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
|||||
Db 247 CAACGACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCATCTTATATGCTC 306

Qy 21 LeuLeuileCysIleIleValMetLeuLeu 30
|||||
Db 307 TTGTTGATCTGCATCATCTGATGCTTCTC 336

RESULT 14

DOGPHL 832 bp mRNA linear MAM 27-APR-1993

LOCUS Dog cardiac phospholamban mRNA, complete cds.

DEFINITION M35393

ACCESSION M35393.1 GI:164045

VERSION phospholamban.

KEYWORDS Canis sp.

SOURCE Canis sp.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 832)

AUTHORS Uyeda, A., Kitano, K., Fujii, J., Kadoya, M., Tada, M., and Tanaka, S.

TITLE Characterization of recombinant cDNA clones for canine cardiac phospholamban

JOURNAL Nucleic Acids Symp. Ser. 17, 121-124 (1986)

MEDLINE 87174860

PUBMED 3562256

COMMENT Original source text: Dog heart, cDNA to mRNA, clone pPLB1.

FEATURES

source

CDS

ORIGIN

Alignment Scores:

Pred. No.:	5,286-09	Length:	832
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-724-532-1 (1-30) x DQFLBA (1-832)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20

DB 247 CAAGCAGCTCAAAATCTTCAGAACCTATTATTAATTTCTGCTCATTTTATATATGCTC 306

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

DB 307 TTGTTGATCTGCATCATGCTGCTTC 336

RSJUT 15

RABPHLAM2 858 bp DNA linear MAM 27-APR-1993

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

Oryctolagus cuniculus (rabbit)

Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 858)

Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and MacLennan,D.H.

Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6

J. Biol. Chem. 266 (18), 11669-11675 (1991)

1828805

COMMENT

FEATURES

source

Original

location/Qualifiers

1..858

/organism="Oryctolagus cuniculus"

/mol_type="genomic DNA"

/db_xref="taxon:9986"

/tissue_id="rabbit genomic"

join(M63600.1:855..943,428..858)

/product="phospholamban"

428..858

/product="phospholamban"

/number=2

524..682

/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"

/codon_start=1

/product="phospholamban"

/protein_id="AA31445.1"

/db_xref="GI:165639"

/translation="MEKVOYLRSAIRRASTIEMPOARONLQNFIFCLILICLL ICIIVMLT"

ORIGIN

Alignment Scores:

Pred. No.:	5,436-09	Length:	858
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-724-532-1 (1-30) x RABPHLAM2 (1-858)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20

DB 590 CAAGCAGCTCAAAACCTCCAGAACCTATTATTCATTTCTGCTCATCTGATATGCTC 649

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

DB 650 CTGCTGATCTGCATCATGCTGCTTC 679

Search completed: July 7, 2005, 18:51:24

Job time : 8380 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 7, 2005, 16:04:14 ; Search time 2134 Seconds
(without alignments)
535.112 Million cell updates/sec

Title: US-10-724-532-1
Perfect score: 150
Sequence: 1 QARQLQNLFLNFCILICLLICILVWML 30

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+g2n.model -DEV=xlh
-Q=/cgn2.1/USPFO/spool/US1074532/runat_07072005_100329_19999/app_query.fasta_1.199
-DB=EST -QFMT=fasta -SUPFIX=p2n.rst -MINMATCH=0.1 -LOOFCOL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US1074532@cgn2.1 1.4352@runat_07072005_100329_19999 -NCPu=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOC
-DEVTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1:	gb_esc1:*
2:	gb_esc2:*
3:	gb_hic:*
4:	gb_esc3:*
5:	gb_esc4:*
6:	gb_esc5:*
7:	gb_esc6:*
8:	gb_g881:*
9:	gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	150	100.0	179	2	BE113353 UI-R-BJ1- BE113353 UI-R-BJ1- AA462116 v972f08.r
2	150	100.0	209	1	AA462116 v972f08.r
3	150	100.0	328	1	AA839963 v66f09.r
4	150	100.0	331	1	AA655419 v14b04.r
5	150	100.0	337	5	BY149365 BY149365 BY149365 BY149365
6	150	100.0	347	1	AA433518 v42f04.r
7	150	100.0	359	5	BY068506 BY068506 BY068506 BY068506
8	150	100.0	362	6	BY770786 BY770786 BY770786 BY770786
9	150	100.0	366	1	AI597561 AI597561 AI597561 v480610.y

10	150	100.0	369	1	AA499852	AA499852 v05g01.r
11	150	100.0	373	6	CB041339	CB041339 4003081.B
12	150	100.0	375	5	BY092385	BY092385 BY092385
13	150	100.0	377	2	BF547322	BF547322 UI-R-C2P-
14	150	100.0	378	2	BF044741	BF044741 BP250001B
15	150	100.0	378	5	BY088220	BY088220 BY088220
16	150	100.0	380	5	BY092582	BY092582 BY092582
17	150	100.0	381	5	BK669692	BK669692 BK669692
18	150	100.0	385	5	BY096259	BY096259 BY096259
19	150	100.0	390	1	AY671547	AY671547 AY671547
20	150	100.0	390	1	AA222425	AA222425 MY18605.r
21	150	100.0	402	1	AI554976	AI554976 UI-R-C2P-
22	150	100.0	417	1	AI322542	AI322542 mh89506.Y
23	150	100.0	419	1	AA655212	AA655212 v13d02.Y
24	150	100.0	425	1	AI467234	AI467234 v480610.x
25	150	100.0	432	1	AA432895	AA432895 v480610.x
26	150	100.0	432	1	AA422326	AA422326 v45b05.r
27	150	100.0	434	5	BY456761	BY456761 BY456761
28	150	100.0	437	1	AI322347	AI322347 mc39e02.Y
29	150	100.0	439	2	BE115006	BE115006 UI-R-BJ1-
30	150	100.0	442	7	CK332692	CK332692 H8210A04-
31	150	100.0	443	5	BY059966	BY059966 BY059966
32	150	100.0	444	1	AI481388	AI481388 v912f03.x
33	150	100.0	448	2	AM226892	AM226892 um63b05.Y
34	150	100.0	449	2	BF394968	BF394968 UI-R-CW0-
35	150	100.0	449	2	BE098177	BE098177 UI-R-BJ1-
36	150	100.0	451	4	BI288911	BI288911 UI-R-CS08
37	150	100.0	452	1	AA499951	AA499951 v906406.r
38	150	100.0	454	2	BE099930	BE099930 UI-R-BJ1-
39	150	100.0	456	1	AA420262	AA420262 v451g02.r
40	150	100.0	469	1	AA466801	AA466801 v490611.r
41	150	100.0	476	2	BF525258	BF525258 UI-R-ACO-
42	150	100.0	480	7	CR471116	CR471116 CR471116
43	150	100.0	482	4	BG223610	BG223610 IM0009808
44	150	100.0	487	4	BG379827	BG379827 UI-R-CS0-
45	150	100.0	490	1	AA435031	AA435031 v606b10.r

ALIGNMENTS

RESULT 1
BE113353/c 179 bp mRNA linear EST 13-UTN-2000
LOCUS UI-R-BJ1-awe-d-04-0-UI-g1 UI-R-BJ1 Rattus norvegicus CDNA clone
DEFINITION UI-R-BJ1-awe-d-04-0-UI 3', mRNA sequence.

ACCESSION BE113353.1 GI:8505458
VERSION BE113353
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 179)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
PUBMED 97044477
COMMENT Contract: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Oligo-dT track not found. Not 1 site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.regen.com)
Seq primer: M13 Forward
POLYA=No.

MGI:662497
Seq primer: -28m13 rev1 ET from Amerham
High quality sequence stop: 73.
Location/Qualifiers

1..328
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Sw18"
/db_xref="taxon:10090"
/clone="IMAGE:1259945"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

Alignment Scores:
Pred. No.: 8,48e-09 Length: 328
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-724-532-1 (1-30) x AA839963 (1-328)

QY 1 GlnAATGAGGlnAsnLeuGlnAsnLeuPheLeuAanPheCysLeuLeuLeuLeuCysLeu 20
|||||
DB 191 CAAGCAGCTCAGAACTCCAGAACCTATTATCAATTTCTGCTCATCTTGATATGCTCG 250
|||||
QY 21 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 30
|||||
DB 251 CTCGATCTGCATCTGATCTGATCTGCTTCG 280
|||||

RESULT 4
LOCUS AA655419 331 bp mRNA linear EST 04-NOV-1997
DEFINITION IMAGE:1211599 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN
(HUMAN); mRNA sequence.

ACCESSION AA655419
VERSION AA655419
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 331)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M.,
Schelling, B., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marras M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMBES Consortium (info@image.lnl.gov) for further information.
MGI:647943

Seq primer: -28m13 rev1 ET from Amerham

High quality sequence stop: 328.
Location/Qualifiers

1..331
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Sw18"
/db_xref="taxon:10090"
/clone="IMAGE:1211599"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

Alignment Scores:
Pred. No.: 8,56e-09 Length: 331
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-724-532-1 (1-30) x AA655419 (1-331)

QY 1 GlnAATGAGGlnAsnLeuGlnAsnLeuPheLeuAanPheCysLeuLeuLeuLeuCysLeu 20
|||||
DB 120 CAAGCAGCTCAGAACTCCAGAACCTATTATCAATTTCTGCTCATCTTGATATGCTCG 179
|||||
QY 21 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 30
|||||
DB 180 CTCGATCTGCATCTGATCTGATCTGCTTCG 209
|||||

RESULT 5
LOCUS BY149365 337 bp mRNA linear EST 10-DEC-2002
DEFINITION BY149365 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930261L14 5', mRNA sequence.

ACCESSION BY149365
VERSION BY149365
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 337)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bul, C.,
Hume, D.A., Quackenbush, J., Schrim, L.M., Kanapin, A., Matcude, H.,
Bacalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brasic, V.,
Chochia, C., Corbani, L.B., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Glas, C., Godzik, A., Gough, J., Grimond, S.,
Gustincich, S., Hirokawa, N., Jackson, R.M., King, B.L., Kana, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konaga, A.,
Kurochkin, I.V., Lee, Y., Lemard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Nunata, K., Okido, T., Pavan, W.J., Petrea, G., Pezole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, J.U., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R., Tomita, M.,
Verardo, R., Wagner, L., Wahlested, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yangisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	22354683
PUBMED	12466851
COMMENT	Contact: Yoshihide Hayashizaki

```

FEATURES
source
location/Qualifiers
1..337
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="193026114"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_1b="RIKEN full-length enriched, 17.5 days embryo
whole body"

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Alignment Scores:	
pred. No.:	8,73e-09
Score:	150.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	5
Length:	33
Matches:	30
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-724-532-1 (1-30) X BY149365 (1-337)

Qy	GllallatrglnslnleuglnaenleupheileasnPhcCysLeuileCysleu 20
Db	219 CAACACGCTCGAATCTCCAGAACCTATTATCAATTTCTGCTATCTTAATGCTG 278
Qy	21 LeuleuileCysleileValMetleuLeu 30
Db	279 CTGCTGATGTCATCATTTGATGAGCTTCTG 308

	RESULT 6					
AA433518						
LOCUS		347 bp	mRNA	linear	EST-29-MAY-1997	
DEFINITION	AA433518	vfi2f04.t1 Soares mouse NMDH Mus musculus CDNA clone IMAGE:846463				
		5' similar to gp:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN) ;,				
		sequence.				
ACCESSION	AA433518					
VERSION	AA433518.1	GI:2130436				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					

TITLE	JOURNAL	COMMENT
REFERENCE AUTHORS	1 (bases 1 to 347)	
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gessel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B., Thaising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Warston,R.	The WashU-HMI Mouse EST Project	
Unpublished (1996)		
Contact: Marra M/Mouse EST Project		

```

FEATURES
source
Location/Qualifiers
1..347
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:846463"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse NBMH"
/note="Vector: pTRT3D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTTACCAATGTGAAGTGGAGCGCGCCGCAAGTTTTTTTTTTTTTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTRT3 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. library
constructed and normalized by Benço Soares and M.Fatima
Bonaldo."

```

Alignment Scores:	
Pred. No.:	9e-09
Length:	3
Matches:	150
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	1

US-10-724-532-1 (1-30) X AA433518 (1-347)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 209 CAAAGCAGTCAGATCTCCAGAACCTATTATCAATTTCTGCTCATCTTGAATAGCTG 268
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.jp/>) for
further details.

FEATURES

source

Location/Qualifiers
1. 362
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U930045G09"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_id="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN

Alignment Scores:

Pred. No.:	9.42e-09	Length:	362
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-724-532-1 (1-30) x BY770786 (1-362)

QY 1 GlnAaArgGlnAaenLeuGlnAaenLeuPheileanPheCysleuileleuileCysleu 20
Db 218 CAAGACGCTCAGAACTCCAGAACTATTATTCATTCTGCTCATCTTGATATGCTG 277

QY 21 LeuLeuileCysleileleValMetleu 30
Db 278 CTGCTGATCTGCATCATCTGATGCTCTG 307

RESULT 9 366 bp mRNA linear EST 21-APR-1999
A1597561
LOCUS v080e10.y1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:806922
DEFINITION 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
sequence.

ACCESSION A1597561
VERSION A1597561.1 GI:4606609
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 366)
REFERENCE Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schuck, R.,
Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCam, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
CONTACT: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watsn.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:483266
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco.

FEATURES

source

Location/Qualifiers
1. 366

ORIGIN

Alignment Scores:
Pred. No.: 9.53e-09 Length: 366
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-724-532-1 (1-30) x A1597561 (1-366)

QY 1 GlnAaArgGlnAaenLeuGlnAaenLeuPheileanPheCysleuileleuileCysleu 20
Db 201 CAAGACGCTCAGAACTCCAGAACTATTATTCATTCTGCTCATCTTGATATGCTG 260

QY 21 LeuLeuileCysleileleValMetleu 30
Db 261 CTGCTGATCTGCATCATCTGATGCTCTG 290

RESULT 10 369 bp mRNA linear EST 01-JUN-1997
AA499852
LOCUS v050g01.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:860496
DEFINITION 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
sequence.

ACCESSION AA499852
VERSION AA499852.1 GI:2234819
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 369)
REFERENCE Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watsn.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:504584
High quality sequence stop: 320.

FEATURES

Location/Qualifiers

1. 320

source

1. .369
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:860496"
 /sex="male"
 /tissue_type="heart"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_11b="Soares mouse NBMH"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 9.61e-09 Length: 369
 Score: 150.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-724-532-1 (1-30) x AA499852 (1-369)

QY 1 GlnAaAgGlnAaenLeuGlnAaenPhelAaenPhcCyleuileuileCysleu 20
 Db 205 CAAGCAGCGTCAAAATCTCCAGAACCTATTATCAATTCCTCATCTGATATGCTCG 264
 QY 21 LeuLeuileCyailelleleValMetLeuLeu 30
 Db 265 CTGCTGATCTGCATCTGATGATGCTTCG 294

RESULT 11
 CB041339 373 bp mRNA linear EST 15-JAN-2003
 LOCUS 4003081 BARC-EMBRAPA 312BOV Bos indicus cDNA clone 312BOV_1A09
 DEFINITION Unknown, mRNA sequence.

ACCESSION CB041339
 VERSION CB041339.1 GI:27760584
 KEYWORDS EST.
 SOURCE Bos indicus (zebu)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 373)
 AUTHORS da Mota,A.F., Sonstegard,T.S., Van Tassel,J.C.P., Matukumalli,L.K., Wood,D.U., Capuco,A.A., Brito,M.A.P., Martinez,M.L., Connor,E.E., Machado,M.A. and Coutinho,L.L.
 TITLE Construction and Characterization of cDNA Libraries Generated from Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos indicus) Cattle

JOURNAL Unpublished (2002)
 COMMENT Contact: Adilson F. da Mota
 Gene Evaluation and Mapping Laboratory
 USDA, ARS, Animal and Natural Resources Institute
 Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA
 Tel: 3015048456
 Fax: 3015048414

Email: amocae@ngj.embrrapa.br
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim_alt '-trim_fast. Vector identified
 by cross match using options -mismatch 12 -mismatch 12

FORWARD: GTTTCACGTCACGACGTTG
 BACKWARD: TGACCGGATACAAATTCACACAG
 Place: 1 row: A column: 09
 Seq primer: GTTTCACGTCACGACGTTG
 High quality sequence stop: 373.
 Location/Qualifiers

source

1. .373
 /organism="Bos indicus"
 /mol_type="mRNA"
 /strain="Brazilian Dairy Gir"
 /db_xref="taxon:9915"
 /clone="312BOV_1A09"
 /sex="female"
 /tissue_type="teat claster and alveoli"
 /cell_type="multiple"
 /dev_stage="involved"
 /lab_host="K-12"
 /clone_11b="BARC-EMBRAPA 312BOV"
 /note="Organ: mammary; Vector: pUC19; Site 1: SmaI; Site 2: SmaI; This mammary-derived cDNA library was created as part of a collaborative project between the ARS Gene Evaluation and Mapping Laboratory and the EMBRAPA Dairy Cattle Research Center under the sponsorship of USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA extracted on 6/8/02 with Invitrogen Superscript II at 37 deg C annealing temperature."

ORIGIN

Alignment Scores:
 Pred. No.: 9.72e-09 Length: 373
 Score: 150.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-724-532-1 (1-30) x CB041339 (1-373)

QY 1 GlnAaAgGlnAaenLeuGlnAaenPhelAaenPhcCyleuileuileCysleu 20
 Db 111 CAAGCAGCGTCAAAATCTCCAGAACCTATTATCAATTCCTCATCTGATATGCTCG 170

QY 21 LeuLeuileCyailelleleValMetLeuLeu 30
 Db 171 TTGCTGATCTGCATCTGATGATGCTTC 200

RESULT 12
 BY092385 375 bp mRNA linear EST 07-DEC-2002
 LOCUS BY092385 RIKEN full-length enriched, 10 days neonate heart Mus
 DEFINITION musculus cDNA clone K630091G17 5', mRNA sequence.

ACCESSION BY092385
 VERSION BY092385.1 GI:26204485
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 375)
 AUTHORS

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Otsu,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bulc,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Mateuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Brdtk,D., Brusik,V., Chochia,C., Corbani,L.E., Cousins,S., Della,E., Dregani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Giesi,C., Godzik,A., Gough,J., Grimond,S., Guerinich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglocz,D.R., Maltale,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perlea,G., Pesole,G.,

ORIGIN

Alignment Scores:

Pred. No.:	9.83e-09	Length:	377
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-724-532-1 (1-30) x BF547322 (1-377)

Qy 1 GlnAaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20

Db 41 CAAGCGCGTCAGAACTCCAGAACTCTTATCAATTTCTGCTCATCTTGATATGCTC 100

Qy 21 LeuLeuIleCysGlleIleIleValMetLeuLeu 30

Db 101 CTGCTGATCTGCATCATGTGATGCTTCTC 130

RESULT 14

BF044741

LOCUS BP250001B10F7 Soares normalized bovine placenta Bos taurus CDNA

DEFINITION clone BP250001B10F7 5', mRNA sequence.

ACCESSION BF044741

VERSION BF044741.1 GI:10761796

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos

1 (bases 1 to 378)

Lewin,H.A., Soares,M.B., Rebelz,M., Pardinas,J., Liu,L. and

Larson,J.H.

Bovine ESTs

Unpublished (2000)

Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL

61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trim: 9:

Cross_match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.

PCR Primers

FORWARD: TATACGACTCACTATAGG

BACKWARD: ATTAACCTCACTAAG

Insert length: 378 Std Error: 0.00

Plate: BP250001B10 row: F column: 7

Seq primer: AGCGGATTAACAATTTTCACAGAA

High quality sequence stop: 378.

Location/Qualifiers

1. 378

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="BP250001B10F7"

/sex="female"

/lab_host="DH10B"

/clone_lib="Soares normalized bovine placenta"

/note="Organ: placenta; Vector: pT733ac; Site 1: EcoRI;

Site 2: NotI; The cDNA library was constructed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806. "

ORIGIN

Alignment Scores:

Pred. No.:	9.86e-09	Length:	378
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-724-532-1 (1-30) x BF044741 (1-378)

Qy 1 GlnAaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20

Db 235 CAAGCAGTCAGAAATCTCAGAACTCTTATCAATTTCTGCTCATCTTGATATGCTC 294

Qy 21 LeuLeuIleCysGlleIleIleValMetLeuLeu 30

Db 295 TTGCTGATCTGCATCATGTGATGCTTCTC 324

RESULT 15

BY088220

LOCUS BY088220 RIKEN full-length enriched, 10 days neonate heart Mus

musculus CDNA clone K630069J15 5', mRNA sequence.

ACCESSION BY088220

VERSION BY088220.1 GI:26203986

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 378)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bule,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matzuda,H.,

Baralov,S., Beisel,K.W., Blake,J.A., Brdtk,D., Brusic,V.,

Chochia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Gimmond,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanaya,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konegaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Malais,L., Marchionni,L., McKenna,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Petrea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Sempile,C.A., Secou,M., Shimada,K.,

Sultana,R., Takekura,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wu,Y., Zavalan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kishikawa,T., Kono,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

Arikawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Saeki,D., Shibata,K.,

Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki

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Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, T., Kikimura, T., Arkawa, T., Carminci, P., Fukuda, S., Miyazawa, K., Murata, K., Ishii, Y., Itoh, M., Komori, H., Miyazaki, A., Muto, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanahi, A., Muramatsu, A., Hayashizaki, Y. Direct Submersion Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences *Mamm. Genome*. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Source

```
Location/Qualifiers
1..378
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="axon:10980"
/cdome="K630069L5"
/tissue_type="heart"
/dev_stage="10 days neonate"
/clome_lib="RIKEN full-length enriched, 10 days neonate
heart"
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ORIGIN

Alignment Scores:

Pred. No.:	9	66e-09	length:	378
Score:	150.00		Matches:	30
Percent Similarity:	100.00%		Conservative:	0
Best local Similarity:	100.00%		Mismatches:	0
Query Match:	100.00%		Indels:	0
DB:	5		gaps:	0

US-10-724-532-1 (1-30) X BY088220 (1-378)

Oy	1	GlnAlaaCGlAAsmLeuInAsnLeuPheIleAsnPheCysLeuIleuIleCysLeu	20
Dd	236	CAGACGCGCAAAATCTCCAGAACCATTTATTACAATTCGGCTCATCTTGAAATGTCTG	295
Oy	21	LeuLeuIleCysIleIleValMetLeuLeu	30
Dd	296	CTGCTGAATCTGCATCATTTGTGAATGCTTCTCG	325

Search completed: July 7, 2005, 19:27:09

Job time : 2144 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 7, 2005, 16:06:22 ; Search time 511 Seconds
(without alignments)
96.063 Million cell updates/sec

Title: US-10-724-532-1
Perfect score: 150
Sequence: 1 QARONQNFNFCLILICLLIICIIIMLL 30

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n model -DRV=rlh
-Q/cgn2_1/USFTO_spool/US10724532/runat_07072005_100330_20013/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=IsaTab -SUFFIX=p2n.rnt -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORMT=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MAP -LARGEBUTTER -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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6: /cgn2_6/prodata/1/ina/backfillseq.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	150	100.0	159	4 US-09-549-872B-9	Sequence 9, Appl
2	150	100.0	159	4 US-09-549-872B-13	Sequence 13, Appl
3	144	96.0	1480	4 US-09-513-9992-10799	Sequence 10799, A
4	144	96.0	1635	4 US-09-949-016-1439	Sequence 1439, Ap
5	144	96.0	16062	4 US-09-949-016-13181	Sequence 13181, A
6	130	86.7	315	3 US-09-124-671-26	Sequence 26, Appl
7	71	47.3	69764	4 US-09-949-016-15638	Sequence 15638, A
8	68	45.3	490	4 US-09-270-767-10524	Sequence 10524, A
9	68	45.3	553	4 US-09-270-767-11139	Sequence 11139, A
10	68	45.3	992	4 US-09-270-767-14599	Sequence 14599, A
11	66	44.0	93920	4 US-09-949-016-12461	Sequence 12461, A
12	66	44.0	93920	4 US-09-949-016-16853	Sequence 16853, A

C 13	64	42.7	601	4 US-09-949-016-136216	Sequence 136216, A
C 14	64	42.7	58356	4 US-09-949-016-15563	Sequence 15563, A
C 15	63	42.0	202001	4 US-09-734-674-3	Sequence 3, Appl
C 16	62.5	41.7	761	1 US-08-477-877B-83	Sequence 83, Appl
C 17	62.5	41.7	761	1 US-08-472-281A-83	Sequence 83, Appl
C 18	62.5	41.7	761	2 US-08-477-989B-83	Sequence 83, Appl
C 19	62.5	41.7	807	1 US-08-472-877B-90	Sequence 90, Appl
C 20	62.5	41.7	807	1 US-08-472-281A-90	Sequence 90, Appl
C 21	62.5	41.7	807	2 US-08-477-989B-90	Sequence 90, Appl
C 22	61	40.7	601	4 US-09-949-016-189393	Sequence 189393, A
C 23	61	40.7	48691	4 US-09-949-016-16308	Sequence 16308, A
C 24	61	40.7	77681	4 US-09-949-016-12710	Sequence 12710, A
C 25	61	40.7	77663	4 US-09-949-016-13751	Sequence 13751, A
C 26	61	40.7	92074	4 US-09-949-016-17153	Sequence 17153, A
C 27	60	40.0	601	4 US-09-949-016-27259	Sequence 27259, A
C 28	60	40.0	601	4 US-09-949-016-27260	Sequence 27260, A
C 29	60	40.0	601	4 US-09-949-016-12818	Sequence 12818, A
C 30	60	40.0	601	4 US-09-949-016-160783	Sequence 160783, A
C 31	60	40.0	601	4 US-09-949-016-160784	Sequence 160784, A
C 32	60	40.0	601	4 US-09-949-016-200644	Sequence 200644, A
C 33	60	40.0	601	4 US-09-949-016-200790	Sequence 200790, A
C 34	60	40.0	12191	4 US-09-949-016-16237	Sequence 16237, A
C 35	60	40.0	25401	4 US-09-949-016-13345	Sequence 13345, A
C 36	60	40.0	32594	4 US-09-949-016-12119	Sequence 12119, A
C 37	60	40.0	32658	4 US-09-949-016-16242	Sequence 16242, A
C 38	60	40.0	152582	4 US-09-949-016-12086	Sequence 12086, A
C 39	60	40.0	152583	4 US-09-949-016-17390	Sequence 17390, A
C 40	60	40.0	152583	4 US-09-949-016-17391	Sequence 17391, A
C 41	60	40.0	183112	4 US-09-949-016-14184	Sequence 14184, A
C 42	60	40.0	192302	4 US-09-949-016-15270	Sequence 15270, A
C 43	59	39.3	1113	4 US-09-248-796A-7619	Sequence 7619, Ap
C 44	59	39.3	1454	4 US-09-270-767-29847	Sequence 29847, A
C 45	59	39.3	2165	2 US-08-263-911-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-549-872B-9
; Sequence 9, Application US/09549872B

; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaen, Richard
; APPLICANT: Gooren, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9

Alignment Scores:

Pred. No.: 4.89e-12
Score: 150.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Matches: 159
Conservative: 30
Mismatches: 0
Indels: 0
Gaps: 0

US-10-724-532-1 (1-30) x US-09-549-872B-9 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTC 126
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 127 TTGCTGATTGTCATCATGTCATGCTTCTC 156
RESULT 2
US-09-549-872B-13
Sequence 13, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/09/549, 872B
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129, 596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 159
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
US-09-549-872B-13
Alignment Scores:
Pred. No.: 4,896-12 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-724-532-1 (1-30) x US-09-549-872B-13 (1-159)
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTC 126
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 127 TTGCTGATTGTCATCATGTCATGCTTCTC 156
RESULT 3
US-09-513-999C-10799
Sequence 10799, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122, 487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799

/ LENGTH: 480
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-513-999C-10799
Alignment Scores:
Pred. No.: 1,076-10 Length: 480
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 4 Gaps: 0
US-10-724-532-1 (1-30) x US-09-513-999C-10799 (1-480)
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 262 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTC 321
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 322 TTGCTGATTGTCATCATGTCATGCTTCTC 351
RESULT 4
US-09-949-016-1439
Sequence 1439, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1439
LENGTH: 1635
TYPE: DNA
ORGANISM: Human
US-09-949-016-1439
Alignment Scores:
Pred. No.: 4,36-10 Length: 1635
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 4 Gaps: 0
US-10-724-532-1 (1-30) x US-09-949-016-1439 (1-1635)
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 248 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTC 307
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 308 TTGCTGATTGTCATCATGTCATGCTTCTC 337
RESULT 5
US-09-949-016-13181
Sequence 13181, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13181
/ LENGTH: 16062
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-13181

Alignment Scores:
Pred. No.: 5,78e-09 Length: 16062
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x US-09-949-016-13181 (1-16062)
QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhCysLeuIleLeuIleCysLeu 20
DB 12674 CAAGCAGCTCAAGCTCAAGCTCAAGCTCAATTCATTCATTCATTCATTCATTCATTC 12733

QY 21 LeuLeuIleCysIleIleValMetLeu 30
DB 12734 TTGCTGATCTGTATCATCTGTGATGCTTCTC 12763

RESULT 6
US-09-124-671-26
/ Sequence 26, Application US/09124671A
/ Patent No. 6160088
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James
/ APPLICANT: Mayhew, Mark
/ APPLICANT: Hoe, Mee
/ TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
/ FILE REFERENCE: 31468
/ CURRENT APPLICATION NUMBER: US/09/124,671A
/ CURRENT FILING DATE: 1998-07-29
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 315
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chimeric human PLB-KDEL
US-09-124-671-26

Alignment Scores:
Pred. No.: 4,67e-09 Length: 315
Score: 130.00 Matches: 26
Percent Similarity: 96.30% Conservative: 0
Best Local Similarity: 96.30% Mismatches: 1
Query Match: 86.67% Indels: 0
DB: 3 Gaps: 0

US-10-724-532-1 (1-30) x US-09-124-671-26 (1-315)
QY 4 GlnAsnLeuGlnAsnLeuPheIleAsnPhCysLeuIleLeuIleCysLeuLeuIle 23
DB 100 CAAGAAGCTCAAGCTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 159

QY 24 CysIleIleValMetLeu 30
```

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DB 160 TGTATCATCTGATGCTTCTC 180

RESULT 7
US-09-949-016-15638
/ Sequence 15638, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15638
/ LENGTH: 69764
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(69764)
/ OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15638

Alignment Scores:
Pred. No.: 135 Length: 69764
Score: 71.00 Matches: 13
Percent Similarity: 64.29% Conservative: 5
Best Local Similarity: 46.43% Mismatches: 10
Query Match: 47.33% Indels: 0
DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x US-09-949-016-15638 (1-69764)
QY 2 AlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhCysLeuIleLeuIleCysLeu 21
DB 61158 GCAAGCAAGCTTCAAAATATATGCAACAATTTTGTATTATTCATTCATTCATTC 61217

QY 22 LeuIleCysIleIleValMetLeu 29
DB 61218 TTGTTGTGTTTTTATTATTCATTTA 61241

RESULT 8
US-09-270-767-10524/C
/ Sequence 10524, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-034
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10524
/ LENGTH: 490
/ TYPE: DNA
/ ORGANISM: Drosophila melanogaster
US-09-270-767-10524

Alignment Scores:
Pred. No.: 1,19 Length: 490
Score: 68.00 Matches: 15
Percent Similarity: 73.91% Conservative: 2
Best Local Similarity: 65.22% Mismatches: 4
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Query Match: 45.33% Indels: 2
DB: 4 Gaps: 1
US-10-724-532-1 (1-30) x US-09-270-767-10524 (1-490)
Qy 10 PheIIeaenPheCysleu-----lleuIIeCysleuLeuIIeCysIIeIIeVal 27
Db 334 TTATATATATTTTATTTATGTTATCTTATTTGTTGTTTATTTGTTGTTGTT 275
Qy 28 MetleuLeu 30
Db 274 TGCCTGTTG 266
RESULT 9
US-09-270-767-11139
; Sequence 11139, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11139
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11139
Alignment Scores:
Pred. No.: 1.37 Length: 553
Score: 68.00 Matches: 15
Percent Similarity: 73.91% Conservative: 2
Best Local Similarity: 65.22% Mismatches: 4
Query Match: 45.33% Indels: 2
DB: 4 Gaps: 1
US-10-724-532-1 (1-30) x US-09-270-767-11139 (1-553)
Qy 10 PheIIeaenPheCysleu-----lleuIIeCysleuLeuIIeCysIIeIIeVal 27
Db 90 TTATATATATTTTATTTATGTTATCTTATTTGTTGTTTATTTGTTGTTGTT 149
Qy 28 MetleuLeu 30
Db 150 TGCCTGTTG 158
RESULT 10
US-09-270-767-14599
; Sequence 14599, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14599
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14599
Alignment Scores:
Pred. No.: 2.66 Length: 992
Score: 68.00 Matches: 15
Percent Similarity: 73.91% Conservative: 2
Best Local Similarity: 65.22% Mismatches: 4
Query Match: 45.33% Indels: 2

DB: 4 Gaps: 1
US-10-724-532-1 (1-30) x US-09-270-767-14599 (1-992)
Qy 10 PheIIeaenPheCysleu-----lleuIIeCysleuLeuIIeCysIIeIIeVal 27
Db 516 TTATATATATTTTATTTATGTTATCTTATTTGTTGTTTATTTGTTGTTGTT 575
Qy 28 MetleuLeu 30
Db 576 TGCCTGTTG 584
RESULT 11
US-09-949-016-12461
; Sequence 12461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12461
; LENGTH: 93920
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12461
Alignment Scores:
Pred. No.: 866 Length: 93920
Score: 66.00 Matches: 8
Percent Similarity: 76.00% Conservative: 11
Best Local Similarity: 32.00% Mismatches: 6
Query Match: 44.00% Indels: 0
DB: 4 Gaps: 0
US-10-724-532-1 (1-30) x US-09-949-016-12461 (1-93920)
Qy 6 leuIIeaenPheIIeaenPheCysleuIIeIIeCysleuLeuIIeCysIIeVal 25
Db 68118 TTAAATATATATGATATATTTTATGCTTATTTAAATATATATTTCTATGCTTA 68177
Qy 26 lleValMetleuLeu 30
Db 68178 TTATGTTTATATATA 68192
RESULT 12
US-09-949-016-16853
; Sequence 16853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012


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Qy      27    Val 27
Db      92176  GTC 92174
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Job time : 550 secs

GenCore version 5.1.6
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Title: US-10-724-532-1

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Maximum Match 100%

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	144	96.0	159	19	US-10-691-412-1
5	144	96.0	159	19	US-10-691-412-1
6	144	96.0	159	19	US-10-691-412-1
7	140	93.3	394	10	US-10-843-611A-162
8	140	93.3	394	10	US-10-843-611A-162
9	139	92.7	380	10	US-10-843-611A-162
10	139	92.7	380	10	US-10-843-611A-162
11	137	91.3	108	20	US-10-724-532-3
12	137	91.3	108	20	US-10-724-532-3
13	137	91.3	135	20	US-10-724-532-5
14	137	91.3	135	20	US-10-724-532-5
15	130	86.7	315	20	US-10-815-514-26
16	130	86.7	315	20	US-10-815-514-26
17	130	86.7	315	20	US-10-815-514-26
18	117	78.0	492	10	US-10-873-594-26
19	116	77.3	407	10	US-10-873-594-26
20	68	45.3	256525	13	US-10-918-995-17377
21	65	43.3	614	20	US-10-357-930-53889
22	65	43.3	43329	13	US-10-087-192-517
23	65	43.3	120581	17	US-10-085-117-247
24	64	42.7	96599	11	US-10-997-722-199
25	63.5	42.3	3673778	16	US-10-424-599-50064
26	63	42.0	1368	18	US-10-424-599-50064
27	63	42.0	1680	20	US-10-729-930-303
28	63	42.0	202001	9	US-10-729-930-303
29	63	42.0	202001	14	US-10-724-990-3
30	63	42.0	202001	24	US-11-061-820-3
31	63	42.0	202002	19	US-10-367-094-192
32	62.5	41.7	397658	9	US-10-813-320-3
33	62.5	41.7	397658	24	US-11-044-879-3
34	62	41.3	409	19	US-10-674-124A-5642
35	62	41.3	457	19	US-10-674-124A-5649
36	62	41.3	34769	18	US-10-221-714A-501
37	62	41.3	62169	19	US-10-332-696-157
38	62	41.3	94512	13	US-10-087-192-985
39	62	41.3	202251	13	US-10-087-192-985
40	61.5	41.0	46675	13	US-10-087-192-985
41	61	40.7	364	19	US-10-674-124A-4970
42	61	40.7	605	13	US-10-027-632-6326
43	61	40.7	605	17	US-10-027-632-6326
44	61	40.7	623	13	US-10-027-632-6326
45	61	40.7	623	17	US-10-027-632-6326

ALIGNMENTS

RESULT 1
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035. US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9906670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15

```
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Alignment Scores:
Pred. No.:      8.98e-11      Length:      159
Score:          150.00        Matches:      30
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%      Indels:       0
DB:             15           Gaps:         0

US-10-724-532-1 (1-30) x US-10-371-101-9 (1-159)

Cy      1 GlnAaagGlnAnleuGlnAnleuPheIleAnPheCyLeuIleLeuIleCyLeu 20
Db      67 CAAGCAGCTCAAAACCTTCAGAACCTTATTCATTTCGTGTCATCTTAATATGCCTC 126

Cy      21 LeuLeuIleCySileIleIleValMetLeuLeu 30
Db      127 TTGCTGATTTGTCATCATCGTATGCTTCTC 156

RESULT 2
US-10-371-101-13
; Sequence 13, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035 US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PIG CDNA
US-10-371-101-13

Alignment Scores:
Pred. No.:      8.98e-11      Length:      159
Score:          150.00        Matches:      30
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    100.00%      Indels:       0
DB:             15           Gaps:         0

US-10-724-532-1 (1-30) x US-10-371-101-13 (1-159)

Cy      1 GlnAaagGlnAnleuGlnAnleuPheIleAnPheCyLeuIleLeuIleCyLeu 20
Db      127 TTGCTGATTTGTCATCATCGTATGCTTCTC 156
```

```
Db      67 CAAGCAGCTCAAAACCTTCAGAACCTTATTCATTTCGTGTCATCTTAATATGCCTC 126

Cy      21 LeuLeuIleCySileIleIleValMetLeuLeu 30
Db      127 TTGCTGATTTGTCATCATCGTATGCTTCTC 156

RESULT 3
US-10-691-412-1
; Sequence 1, Application US/10691412
; Publication No. US20040191802A1
; GENERAL INFORMATION:
; APPLICANT: Kranaas, Evangelia G.
; APPLICANT: Kodra, Haghsni
; TITLE OF INVENTION: Phospholamban Polymorphisms and Methods of Assessment
; FILE REFERENCE: 10738-47
; CURRENT APPLICATION NUMBER: US/10/691,412
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Human
US-10-691-412-1

Alignment Scores:
Pred. No.:      5.35e-10      Length:      159
Score:          144.00        Matches:      29
Percent Similarity: 96.67%    Conservative: 0
Best Local Similarity: 96.67%  Mismatches:  1
Query Match:    96.00%      Indels:       0
DB:             19           Gaps:         0

US-10-724-532-1 (1-30) x US-10-691-412-1 (1-159)

Cy      1 GlnAaagGlnAnleuGlnAnleuPheIleAnPheCyLeuIleLeuIleCyLeu 20
Db      67 CAAGCAGCTCAAAAGCTACAGAACTATTATTCATTTCGTGTCATCTTAATATGCTC 126

Cy      21 LeuLeuIleCySileIleIleValMetLeuLeu 30
Db      127 TTGCTGATCTGTATCATCATCGTATGCTTCTC 156

RESULT 4
US-09-918-995-4045
; Sequence 4045, Application US/09918995
; Publication No. US2003007623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4045
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(525)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4045

Alignment Scores:
Pred. No.:      2.39e-09      Length:      525
Score:          144.00        Matches:      29
Percent Similarity: 96.67%    Conservative: 0
Best Local Similarity: 96.67%  Mismatches:  1
```

```
Query Match: 96.00% Indels: 0
DB: 10 Gaps: 0
US-10-724-532-1 (1-30) x US-09-918-995-4045 (1-525)

QY 1 GlnAaTgGlnAaLnLeuGlnAaLnLeuPheIleAaPheCysLeuIleCysLeu 20
    |||||
DB 376 CAAGCAGCTCAAAAGCTACAGATCTATTATCAATTCTGCTCATCTTAATATGCTTC 435

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
    |||||
DB 436 TTGCTGATCTGTATCATCTGATGCTTC 465

RESULT 5
US-09-873-367C-162
; Sequence 162, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-162

Alignment Scores:
Pred. No.: 9,936-09 Length: 1635
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-873-367C-162 (1-1635)

QY 1 GlnAaTgGlnAaLnLeuGlnAaLnLeuPheIleAaPheCysLeuIleCysLeu 20
    |||||
DB 248 CAAGCAGCTCAAAAGCTACAGATCTATTATCAATTCTGCTCATCTTAATATGCTTC 307

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
    |||||
DB 308 TTGCTGATCTGTATCATCTGATGCTTC 337

RESULT 6
US-10-843-641A-162
; Sequence 162, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
```

```
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-162

Alignment Scores:
Pred. No.: 9,936-09 Length: 1635
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 21 Gaps: 0

US-10-724-532-1 (1-30) x US-10-843-641A-162 (1-1635)

QY 1 GlnAaTgGlnAaLnLeuGlnAaLnLeuPheIleAaPheCysLeuIleCysLeu 20
    |||||
DB 248 CAAGCAGCTCAAAAGCTACAGATCTATTATCAATTCTGCTCATCTTAATATGCTTC 307

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
    |||||
DB 308 TTGCTGATCTGTATCATCTGATGCTTC 337

RESULT 7
US-09-918-995-4217
; Sequence 4217, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4217
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(394)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4217
```

```
Alignment Scores:
Pred. No.: 5.48e-09 Length: 394
Score: 140.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 93.33% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-4217 (1-394)

Qy 1 GlnAaagglnaenleuglnasnleupheilleasnphcysleuileleuilecysleu
Db 248 CAAGCAGCTCAAAAGCTACAGAACTATTATCAATTCTGTCTCATCTTAATATGCTC 307

Qy 21 LeuenuleCySillelleValMetleu 30
Db 308 TTGCTGATCTGTATCATCGCGATGCTTCTC 337

RESULT 8
US-09-918-995-5377
; Sequence 5377, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5377
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(487)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-5377

Alignment Scores:
Pred. No.: 7.15e-09 Length: 487
Score: 140.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 93.33% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-5377 (1-487)

Qy 1 GlnAaagglnaenleuglnasnleupheilleasnphcysleuileleuilecysleu
Db 318 CAAGCAGCTCAAAAGCTACAGAACTATTATCAATTCTGTCTCATCTTAATATGCTC 377

Qy 21 LeuenuleCySillelleValMetleu 30
Db 378 TTGCTGATCTGTATCATCGCGATGCTTCTC 407

RESULT 9
US-09-918-995-3950
; Sequence 3950, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
```

```
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3950
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(380)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-3950

Alignment Scores:
Pred. No.: 7.05e-09 Length: 380
Score: 139.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 92.67% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-3950 (1-380)

Qy 1 GlnAaagglnaenleuglnasnleupheilleasnphcysleuileleuilecysleu
Db 248 CAAGCAGCTCAAAAGCTACAGAACTATTATCAATTCTGTCTCATCTTAATATGCTC 307

Qy 21 LeuenuleCySillelleValMetleu 30
Db 308 TTGCTGATCTGTATCATCGCGATGCTTCTC 337

RESULT 10
US-09-918-995-5235
; Sequence 5235, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5235
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(418)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-5235

Alignment Scores:
Pred. No.: 7.95e-09 Length: 418
Score: 139.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 92.67% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-5235 (1-418)

Qy 1 GlnAaagglnaenleuglnasnleupheilleasnphcysleuileleuilecysleu
Db 222 CAAGCAGCTCAAAAGCTACAGAACTATTATCAATTCTGTCTCATCTTAATATGCTC 281

Qy 21 LeuenuleCySillelleValMetleu 30
Db 282 TTGCTGATCTGTATCATCGCGATGCTTCTC 311
```

```
RESULT 11
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Alignment Scores:
Pred. No.: 2,64e-09 Length: 108
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-724-532-3 (1-108)
QY 1 GlnAaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
DB 19 CAGGCCAGGACGACCTCCAGAAATGCTTCATGCTTTTGTCTGATTCATCTGCGCTC 78
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
DB 79 CTGCTGATTGCAATATGCTCATGCTGCTCG 108

RESULT 12
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Alignment Scores:
Pred. No.: 2,64e-09 Length: 108
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-724-532-4 (1-108)
QY 1 GlnAaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
DB 19 CAGGCCAGGACGACCTCCAGAAATGCTTCATGCTTTTGTCTGATTCATCTGCGCTC 78
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
DB 79 CTGCTGATTGCAATATGCTCATGCTGCTCG 108

RESULT 13
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Alignment Scores:
Pred. No.: 3,49e-09 Length: 135
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-724-532-5 (1-135)
QY 1 GlnAaArgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
DB 31 CAGGCCAGGACGACCTCCAGAAATGCTTCATGCTTTTGTCTGATTCATCTGCGCTC 90
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
DB 91 CTGCTGATTGCAATATGCTCATGCTGCTCG 120

RESULT 14
US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

Alignment Scores:
Pred. No.: 3,49e-09 Length: 135
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0
```

US-10-724-532-1 (1-30) x US-10-724-532-6 (1-135)

OY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20

Db 105 CAGGCCAGGCAGAACCTCCAGAAAGCTTTCATGCTTTTGGTGAATTCATCTGCTGCTC 46

OY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

Db 45 CTGCTGATTTGTCATTTATGTCATGCTCCTG 16

RESULT 15

US-10-815-514-26

; Sequence 26, Application US/10815514

; Publication No. US20040204361A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James

; APPLICANT: Mayhew, Mark

; APPLICANT: Hoe, Mee

; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS

; FILE REFERENCE: 31488

; CURRENT APPLICATION NUMBER: US/10/815,514

; CURRENT FILING DATE: 2004-03-31

; PRIOR APPLICATION NUMBER: US/09/696,872

; PRIOR FILING DATE: 2000-10-26

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 26

; LENGTH: 315

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chimeric human PLB-KDEL

US-10-815-514-26

Alignment Scores:

Pred. No.: 8.1e-08 Length: 315

Score: 130.00 Matches: 26

Percent Similarity: 96.30% Conservative: 0

Best Local Similarity: 96.30% Mismatches: 1

Query Match: 86.67% Indels: 0

DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-815-514-26 (1-315)

OY 4 GlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeuLeuLeuIle 23

Db 100 CAAAGCTACGAAATCTATTATCAATTCGTCTCATCTTAATAATGTCCTTGCTGATC 159

OY 24 CysIleIleValMetLeuLeu 30

Db 160 TGTATCATGCGTATGCTCTTC 180

Search completed: July 7, 2005, 20:34:06
Job time : 424 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 999.333 Seconds
(without alignments)
5236.654 Million cell updates/sec

Title: US-10-724-532-3
Perfect score: 108
Sequence: 1 atgcacgagagaagcctca.....gcatatcgcacgctcctg 108

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53.4	48.5	858	4	RABPHLAM2
2	53.4	48.5	2841	4	OCBPPLAM
3	50.8	47.0	159	6	BD247907
4	50.8	47.0	159	6	BD247911
5	50.8	47.0	159	6	AR302003
6	50.8	47.0	159	6	AR302007
7	50.8	47.0	159	6	AX040487
8	50.8	47.0	159	6	AX040491
9	50.8	47.0	737	4	SSPLB
10	50.2	46.5	159	10	S95853
11	50.2	46.5	386	10	S95849
12	50.2	46.5	701	10	RNPPLAMB
13	50.2	46.5	1786	10	RATPHOLA02
14	50.2	46.5	223728	2	AC097906
15	50.2	46.5	231910	2	AC128365
16	47.6	44.1	130240	5	BX276081
17	47	43.5	648	10	BC061097
18	47	43.5	940	10	S46792
19	47	43.5	79895	2	AC100317

20	47	43.5	177018	2	AC099716	AC099716 Mus muscu
21	46.8	43.3	133901	5	BX537355	BX537355 Zebrafish
22	46.4	43.0	3312	5	CHKPLB	M59039 Chicken car
23	46.4	43.0	3423	5	CHKPLB2	M59038 Chicken pho
24	46.4	42.6	306	6	C0447405	C0447405 Sequence
25	46.4	42.6	323	9	HMPPLAM	M60411 Human phosp
26	46.4	42.6	480	6	AX894936	AX894936 Sequence
27	46.4	42.6	480	6	BD030469	BD030469 Sequence
28	46.4	42.6	980	9	HSP1862	AF177674 Homo sapi
29	46.4	42.6	1635	6	C0718671	C0718671 Sequence
30	46.4	42.6	1635	6	AX329653	AX329653 Sequence
31	46.4	42.6	1635	9	HMPPLAM	M63603 Human phosp
32	46.4	42.6	1691	9	BC005269	BC005269 Homo sapi
33	46.4	42.6	60797	2	AL355356	AL355356 Homo sapi
34	46.4	42.6	66092	2	AL136974	AL136974 Homo sapi
35	46.4	42.6	150290	9	HS50914	Z99496 Human DNA s
36	44.4	41.1	314	4	AY514751	AY514751 Canis fam
37	44.4	41.1	832	4	DOGPHL	M16012 Canine card
38	44.4	41.1	832	4	DOGPLBA	M35393 Dog cardiac
39	44.4	41.1	2614	4	CEPHLX	Y00399 Dog phospho
40	43.6	40.4	315	6	AR121629	AR121629 Sequence
41	36	33.3	147419	9	HS738P1	AL031736 Human DNA
42	33.2	30.7	204114	2	AC108810	AC108810 Mus muscu
43	32.8	30.4	1593	9	AK098521	AK098521 Homo sapi
44	32.8	30.4	1893	9	HSR21SPA	X98294 Homo sapien
45	32.8	30.4	2254	9	AK125620	AK125620 Homo sapi

ALIGNMENTS

RESULT 1	RABPHLAM2	858 bp	DNA	Linear	MAM 27-APR-1993
LOCUS	Rabbit phospholamban gene, partial exon 2.				
DEFINITION	Rabbit phospholamban gene, partial exon 2.				
ACCESSION	M63601.1	GI:165636			
VERSION	M63601.1	GI:165636			
KEYWORDS	phospholamban.				
SEGMENT	2 of 3				
SOURCE	Oryctolagus cuniculus (rabbit)				
ORGANISM	Oryctolagus cuniculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
AUTHORS	Fujii J., Zarain-Herzberg, A., Willard, H. F., Tada, M. and MacLennan, D. H.				
TITLE	Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6				
JOURNAL	J. Biol. Chem. 266 (18), 11669-11675 (1991)				
MEDLINE	91268032				
PUBMED	1828805				
COMMENT	Original source text: Rabbit DNA.				
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source	1..858				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:9986"				
	/tissue_1b="rabbit genomic"				
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mRNA	/product="phospholamban"				
	428..858				
exon	/product="phospholamban"				
	/number=2				
CDS	524..682				
	/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"				
	/codon_start=1				
	/product="phospholamban"				
	/protein_id="AA31445.1"				
	/db_xref="GI:165639"				
	/translation="MEKVYLFTRSAIRRASTTEMPOARQNLQNLFINFCILLCILL				
	ICITVML"				

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Best Local Similarity 69.6%; Pred. No. 2.2e-06;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 TGAAGAGGCGCTCAGCGCAGACCTCCAGAACTCTTCATTCGCTTTTGTCTCAT 65
Db 577 TGAATGCGCTCAACAGACGTCGCAAAACCTCAGAACTTATTCATTCGTCTCAT 636
Qy 66 TCTCATTCGCGCTCGCTGATTTGATATGTCATGCTGCT 107
Db 637 CTGTATATGTCCTCGCTGATCTGCATCATGCTCATGCTTCT 678

RESULT 2
OCPHAM
LOCUS OCPHAM 2841 bp mRNA linear MAM 24-JUL-1992
DEFINITION O. cuniculus mRNA for phospholamban.
ACCESSION Y00761
VERSION Y00761.1 GI:1661
KEYWORDS phospholamban.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2841)
AUTHORS Fujii, J., Lytton, J., Tada, M. and MacLennan, D.H.
TITLE Rabbit cardiac and slow-twitch muscle express the same
JOURNAL FEBS Lett. 227 (1), 51-55 (1988)
MEDLINE 8811222
PUBMED 2962883
FEATURES
source location/Qualifiers
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/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVQYLRSAIRASTIEMPOQARQNIQNLFNFCILICLL
ICITVML"

ORIGIN
Query Match 48.5%; Score 52.4; DB 4; Length 2841;
Best Local Similarity 69.6%; Pred. No. 2.5e-06;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 TGAAGAGGCGCTCAGCGCAGACCTCCAGAACTCTTCATTCGCTTTTGTCTCAT 65
Db 231 TGAATGCGCTCAACAGACGTCGCAAAACCTTATTCATTCGTCTCAT 290
Qy 66 TCTCATTCGCGCTCGCTGATTTGATATGTCATGCTGCT 107
Db 291 CTGTATATGTCCTCGCTGATCTGCATCATGCTCATGCTTCT 332

RESULT 3
BD247907
LOCUS BD247907 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE Sus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 159)

AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV
COMMENT OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1..159
FT location/Qualifiers
1..159
/organism="Sus sp. (pig)".
FEATURES
source location/Qualifiers
1..159
/organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"

ORIGIN
Query Match 47.0%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 6e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 6 TGAAGAGGCGCTCAGCGCAGACCTCCAGAACTCTTCATTCGCTTTTGTCTCAT 65
Db 54 TGAATGCGCTCAACAGACGTCGCAAAACCTTCAGAACTTATTCATTCGTCTCAT 113
Qy 66 TCTCATTCGCGCTCGCTGATTTGATATGTCATGCTGCT 107
Db 114 CTATATATGCTCTTGCTGATTTGCATCATGCTGATGCTTCT 155

RESULT 4
BD247911
LOCUS BD247911 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE Sus sp.
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV
COMMENT OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG PLB cDNA FH
FH Key Location/Qualifiers
FT source 1..159
FT location/Qualifiers
1..159
/organism="Artificial Sequence".
FEATURES
source location/Qualifiers
1..159
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 47.0%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 6e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 205.111 Seconds

(without alignments)
3117.004 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108
Sequence: 1 atgcacgagagagagcctca.....gcattatcgcacgctctcg 108

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_16Dec04:*
2: geneeqn1980s:*
3: geneeqn1990s:*
4: geneeqn2000s:*
5: geneeqn2001s:*
6: geneeqn2002s:*
7: geneeqn2003s:*
8: geneeqn2004s:*
9: geneeqn2005s:*
10: geneeqn2006s:*
11: geneeqn2007s:*
12: geneeqn2008s:*
13: geneeqn2009s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	50.8	47.0	159	3	AAC64967	AAC64967 Pig phosp
2	50.2	46.5	701	10	ADB53082	ADB53082 Primary r
3	46.6	42.6	159	13	ADR97285	ADR97285 Human rho
4	46.6	42.6	306	6	ABN22344	ABN22344 Human ORF
5	46.6	42.6	480	3	AAC06724	AAC06724 Human sec
6	46.6	42.6	525	9	ACH16833	ACH16833 Human adu
7	46.6	42.6	1635	6	ABL61825	ABL61825 Color ade
8	46.6	42.6	1635	12	ADN04087	ADN04087 Antiporci
9	46.6	42.6	1712	12	ADP21384	ADP21384 Gene PLN
10	45	41.7	380	9	ACH16738	ACH16738 Human adu
11	45	41.7	418	9	ACH18023	ACH18023 Human adu
12	44.4	41.1	394	9	ACH17005	ACH17005 Human adu
13	44.4	41.1	487	9	ACH18165	ACH18165 Human adu
14	43.6	40.4	312	3	AAZ50498	AAZ50498 KDEL rece
15	41.2	38.1	407	9	ACH16630	ACH16630 Human adu
16	38	35.2	492	9	ACH30165	ACH30165 Human tes
17	36	33.3	147419	6	ABK83574	ABK83574 Human COL
18	32.8	30.4	652	6	ABG60653	ABG60653 Human COL
19	32.8	30.4	1896	12	ADP07907	ADP07907 Human RAD
20	32.8	30.4	2419	5	ADL62294	ADL62294 Human ova

C 21	32.8	30.4	2422	10	ADC37617	ADC37617 Human nuc
C 22	32.8	30.4	3647	6	ABK83658	ABK83658 Human CDN
C 23	32.8	30.4	3647	10	ADP81412	ADP81412 Leukaemia
C 24	32.8	30.4	3647	13	ADP25399	ADP25399 Breast ca
C 25	32.8	30.4	3647	13	ACN38837	ACN38837 Tumour-as
C 26	32.8	30.4	3708	2	AAZ77530	AAZ77530 Human ova
C 27	32.8	30.4	3748	3	AAZ77586	AAZ77586 Human can
C 28	32.8	30.4	3925	12	ADQ21778	ADQ21778 Human eof
C 29	32	29.6	6481	4	AA159183	AA159183 Human pol
C 30	32	29.6	6481	5	ADQ99406	ADQ99406 DNA encod
C 31	32	29.6	6481	9	ADB49166	ADB49166 Novel hum
C 32	32	29.6	6536	3	AAZ75801	AAZ75801 Human ORF
C 33	32	29.6	10625	5	AAZ85836	AAZ85836 Nucleotid
C 34	32	29.6	10625	6	AA141031	AA141031 DNA encod
C 35	31.2	28.9	473	13	ADQ79072	ADQ79072 Novel can
C 36	30.4	28.1	1938	11	ACN44341	ACN44341 Mouse mRN
C 37	30.4	28.1	2175	2	AAZ24906	AAZ24906 Mouse eio
C 38	30.2	28.0	639	8	ABT14895	ABT14895 Pathogen
C 39	30.2	28.0	639	8	ACF73801	ACF73801 Staphyloc
C 40	30	27.8	415	4	AA113308	AA113308 Probe #32
C 41	30	27.8	415	4	ABA55007	ABA55007 Human foe
C 42	30	27.8	415	4	AA134661	AA134661 Probe #33
C 43	30	27.8	415	4	ABA44562	ABA44562 Human bre
C 44	30	27.8	415	4	ABA24770	ABA24770 Probe #32
C 45	30	27.8	415	4	AAK28730	AAK28730 Human bon

ALIGNMENTS

RESULT 1	
AAC64967	
ID AAC64967 standard; CDNA; 159 BP.	
XX	
AC AAC64967;	
XX	
DT 09-FEB-2001 (first entry)	
XX	
DE Pig phospholamban cDNA.	
XX	
KW Pig, sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;	
KM cardiac hypertrophy; heart failure; hypertension; Darter-White disease;	
KM Brody's disease; diabetes; ss.	
XX	
OS Sus scrofa.	
XX	
PN GB2349217-A.	
XX	
PD 25-OCT-2000.	
XX	
PF 14-APR-2000; 2000GB-00009363.	
XX	
PR 15-APR-1999; 99GB-00008670.	
PR 15-APR-1999; 99US-0129596P.	
PR 01-JUN-1999; 99GB-00012736.	
XX	
PA (DEWG-) DEWGEN NV.	
XX	
PI Zwaal R, Groenen J, Bogaert T;	
XX	
DR WPI; 2000-658082/64.	
XX	
PT Identifying modulators of sarco/endoplasmic reticulum calcium ATPase,	
PT useful potentially for treating disorders of calcium homeostasis, e.g.	
PT cardiac hypertrophy.	
XX	
PS Disclosure; Fig 11; 108pp; English.	
XX	
CC The present invention is concerned with methods of using C. elegans to	
CC identify compounds which are capable of up- and down-regulating the	
CC activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This	
CC protein is involved in cell signalling, and elevated levels affect	
CC cellular processes such as contraction, secretion and cell cycling. The	

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hypertension, diabetes, Darier-White disease and Brody's disease
XX Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;
SO
Query Match 47.0%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.3e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 6 TGAGAGAGGCTCAGGCGCAGACCTCCAGAAATGCTTTCATTCCTTTTGTGAT 65
DB 54 TGAATGCTCCAGCAGACGCTCAAACTTCAGAACTTATTCATTTCTGTCTAT 113
OY 66 TCTCATCTGCTCCTCGTGTGATTTGCATTTATGCTGCTCT 107
DB 114 CTTATATGCTCTTCTGCTGATTTGCATCATGCTGATGCTTCT 155
RESULT 2
ID ADB53082 standard; DNA; 701 BP.
XX ADB53082;
XX
DT 04-DEC-2003 (first entry)
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.
XX
XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX toxicity marker; toxicity progression; drug screening;
XX primary rat hepatocyte toxicity modelling; gene; db.
XX
OS Rattus norvegicus.
XX
XX WO2003065993-A2.
XX
XX
PD 14-AUG-2003.
XX
XX
PP 04-FEB-2003; 2003WO-US003482.
XX
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371135P.
PR 11-APR-2002; 2002US-0371413P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
XX Elashoff M;
XX
XX MPI; 2003-731472/69.
XX
XX
XX Determining if a compound induces a toxic effect on a tissue or cell, for
XX identifying hepatotoxic compounds, comprises comparing a gene expression
XX profile of a tissue or cell sample to a database of Tox mean and non-Tox
XX mean values.
XX
XX Claim 44; SEQ ID NO 3624; 874bp; English.

XX
XX The present invention describes a method for determining whether a
XX compound induces a toxic effect on a tissue or cell. The method comprises
XX preparing a gene expression profile of a tissue or cell sample exposed to
XX the compound, and comparing the gene expression profile to a database
XX comprising data or information on the Tox mean and non-Tox mean value.
XX The method is useful for predicting or identifying at least one toxic
XX effect, particularly hepatotoxicity, of a test or unknown compound. The
XX genes listed in the specification are useful as diagnostic or toxicity
XX markers for the prediction or identification of the physiological state
XX of tissue or cell sample that has been exposed to a compound, or to
XX identify or predict the toxic effects of a compound or an agent. These
XX may also be used as markers for monitoring toxicity progression or for
XX drug screening. The present sequence represents a primary rat hepatocyte
XX toxicity modelling related gene sequence from the present invention.
XX
XX Sequence 701 BP; 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;
SO
Query Match 46.5%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 8.1e-06;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
OY 6 TGAGAGAGGCTCAGGCGCAGACCTCCAGAAATGCTTTCATTCCTTTTGTGAT 65
DB 227 TGAATGCTCCAGCAGACGCTCAAACTTCAGAACTTATTCATTTCTGTCTAT 286
OY 66 TCTCATCTGCTCCTCGTGTGATTTGCATTTATGCTGCTCTG 108
DB 287 CTTGATATGCTCTTCTGCTGATATGATCATCATGTGATGCTTCTG 329
RESULT 3
ID ADR97285 standard; DNA; 159 BP.
XX ADR97285;
XX
XX
DT 16-DEC-2004 (first entry)
DE Human phospholamban polymorphism fragment DNA.
XX
XX
XX ds; human; phospholamban; polymorphism; cardiovascular disease.
XX
XX Homo sapiens.
XX
XX US2004191802-A1.
XX
XX
PD 30-SEP-2004.
XX
XX
PP 22-OCT-2003; 2003US-00691412.
XX
XX
PR 22-OCT-2002; 2002US-0420295P.
XX
XX
PA (KRAN/) KRANTAS B G.
PA (HAGH/) HAGHIGHI K.
XX
XX
PI Krantias EG, Haghighi K;
XX
XX MPI; 2004-689841/67.
XX
XX
XX Phospholamban polymorphism assessment in individual, for determining risk
XX for developing cardiovascular disease, by comparing analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence.
XX
XX Claim 15; SEQ ID NO 1; 15bp; English.
XX
XX
XX The invention relates to a method of phospholamban polymorphism
XX assessment in an individual which comprises comparing the analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence to determine whether the individual carries a
XX phospholamban polymorphism. The methods and phospholamban polymorphism
XX fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 / Search time 1353.33 seconds
(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-3
Perfect score: 108
Sequence: 1 atgcacgagagaagcctca.....gcattatcgcacgctctcg 108

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est1.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	50.8	47.0	381	5	BX669692 BX669692
2	50.8	47.0	702	5	BX922974 BX922974
3	50.8	47.0	724	5	BX674983 BX674983
4	50.8	47.0	740	5	BX924154 BX924154
5	50.8	47.0	758	5	BX923697 BX923697
6	50.8	47.0	811	7	CK449263 CK449263
7	50.2	46.5	179	2	BE113353 BE113353
8	50.2	46.5	377	2	BF547322 BF547322
9	50.2	46.5	417	1	AI322542 AI322542
10	50.2	46.5	439	2	BE115006 BE115006
11	50.2	46.5	449	2	BE098177 BE098177
12	50.2	46.5	449	2	BE098177 BE098177
13	50.2	46.5	451	4	BI288911 BI288911
14	50.2	46.5	454	4	BE099930 BE099930
15	50.2	46.5	476	2	BF525258 BF525258
16	50.2	46.5	480	7	CR471116 CR471116
17	50.2	46.5	487	1	AI603160 AI603160
18	50.2	46.5	498	1	AI603160 AI603160
19	50.2	46.5	511	4	BF395370 BF395370
20	50.2	46.5	513	4	BI296789 BI296789
21	50.2	46.5	518	2	BE112568 BE112568
22	50.2	46.5	527	2	BF395607 BF395607
23	50.2	46.5	528	2	BF395670 BF395670
24	50.2	46.5	540	2	BF395398 BF395398

c	25	50.2	46.5	575	4	BI290034	BI290034	UI-R-DKO-
	26	50.2	46.5	589	2	BF525010	BF525010	UI-R-ABO-
c	27	50.2	46.5	608	1	AI103929	AI103929	EST13218
	28	50.2	46.5	699	7	CK358482	CK358482	AGENCOURT
	29	50.2	46.5	710	7	CK359590	CK359590	AGENCOURT
	30	50.2	46.5	718	7	CK358464	CK358464	AGENCOURT
	31	50.2	46.5	719	7	CK356296	CK356296	AGENCOURT
	32	50.2	46.5	731	7	CK357243	CK357243	AGENCOURT
	33	50.2	46.5	737	7	CK357232	CK357232	AGENCOURT
	34	50.2	46.5	738	7	CK355359	CK355359	AGENCOURT
	35	50.2	46.5	738	7	CK357123	CK357123	AGENCOURT
	36	50.2	46.5	744	7	CK356439	CK356439	AGENCOURT
	37	50.2	46.5	744	7	CK357747	CK357747	AGENCOURT
	38	50.2	46.5	745	7	CK355314	CK355314	AGENCOURT
	39	50.2	46.5	745	7	CK356371	CK356371	AGENCOURT
	40	50.2	46.5	748	7	CK359219	CK359219	AGENCOURT
	41	50.2	46.5	754	7	CK355445	CK355445	AGENCOURT
	42	50.2	46.5	758	7	CK355453	CK355453	AGENCOURT
	43	50.2	46.5	758	7	CK357746	CK357746	AGENCOURT
	44	50.2	46.5	762	7	CK359188	CK359188	AGENCOURT
	45	50.2	46.5	764	7	CK357447	CK357447	AGENCOURT

ALIGNMENTS

RESULT 1
BX669692
LOCUS
DEFINITION BX669692 Sus scrofa library. (scac) Sus scrofa cDNA clone
scac00281.c.02 5prim, mRNA sequence.
ACCESSION BX669692
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 381)
REFERENCE
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
CONTACT: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@journ.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0028 row: C column: 2.

FEATURES

source

Location/Qualifiers
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/tissue_type="mixed"
/clone_lib="Sus scrofa library (scac)"
/note="Vector: pTRIP-pac vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN
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47.0%; Score 50.8; DB 5; Length 381;

Best Local Similarity 68.6%; Pred. No. 0.00012;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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DB 82 TGAATGCTCAACAGACGCAAAACCTTCAGAACCTATTATCAATTCGTGTCAT 141
OY 66 TCTCATCTGCTCCTGCTGATTCGATTCATTCGTCATGCTCT 107
DB 142 CTTAATATGCTCTTCTGCTGATTCATCATCTGATGCTTCT 183

RESULT 2
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LOCUS BX922974
DEFINITION BX922974 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION BX922974
VERSION BX922974
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 702)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
Cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
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FEATURES
source

ORIGIN

Query Match 47.0%; Score 50.8; DB 5; Length 702;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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OY 66 TCTCATCTGCTCCTGCTGATTCGATTCATTCGTCATGCTCT 107
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RESULT 3

BX674983
LOCUS BX674983
DEFINITION BX674983 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION BX674983
VERSION BX674983
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 724)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
Cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
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/note="Vector: pT73D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

FEATURES
source

ORIGIN

Query Match 47.0%; Score 50.8; DB 5; Length 724;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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DB 237 TGAATGCTCAACAGACGCAAAACCTTCAGAACCTATTATCAATTCGTGTCAT 296
OY 66 TCTCATCTGCTCCTGCTGATTCGATTCATTCGTCATGCTCT 107
DB 297 CTTAATATGCTCTTCTGCTGATTCATCATCTGATGCTTCT 338

RESULT 4
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LOCUS BX924154
DEFINITION BX924154 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION BX924154
VERSION BX924154
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 740)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 61.7778 Seconds
(without alignments)
2860.541 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.8	47.0	159	4	US-09-549-872B-9 Sequence 9, Appl
2	50.8	47.0	159	4	US-09-549-872B-13 Sequence 13, Appl
3	46	42.6	1480	4	US-09-513-999C-10799 Sequence 10799, A
4	46	42.6	1635	4	US-09-949-016-1439 Sequence 1439, Ap
5	46	42.6	16062	4	US-09-949-016-13181 Sequence 13181, A
6	43.6	40.4	315	3	US-09-124-671-26 Sequence 26, Appl
7	32	29.6	6481	4	US-09-620-312D-1076 Sequence 1076, Ap
8	30.4	28.1	2175	4	US-08-914-999-3 Sequence 3, Appl
9	30.2	28.0	74353	4	US-09-949-016-15336 Sequence 15336, A
10	29	26.9	4474	4	US-09-513-999C-1161 Sequence 1161, Ap
11	29	26.9	1123	3	US-09-188-930-28 Sequence 28, Appl
12	29	26.9	1123	3	US-09-188-930-203 Sequence 203, App
13	29	26.9	1123	3	US-09-312-283C-28 Sequence 28, Appl
14	29	26.9	1123	3	US-09-312-283C-203 Sequence 203, Appl
15	28.8	26.7	879	4	US-09-489-039A-5041 Sequence 5041, Ap
16	28.4	26.3	162914	4	US-09-949-016-15578 Sequence 15578, A
17	27.8	25.7	72	3	US-08-945-734-11 Sequence 11, Appl
18	27.8	25.7	72	3	US-09-258-797-11 Sequence 11, Appl
19	27.8	25.7	72	5	PCT-US96-09451-11 Sequence 11, Appl
20	27.8	25.7	568	4	US-08-956-171E-999 Sequence 999, App
21	27.8	25.7	568	4	US-08-781-986A-999 Sequence 999, App
22	27.8	25.7	1920	3	US-09-160-496-4 Sequence 4, Appl
23	27.8	25.7	48313	4	US-09-349-016-17088 Sequence 17088, A
24	27.8	25.7	65424	4	US-09-949-016-12426 Sequence 12426, A
25	27.6	25.6	601	4	US-09-949-016-202802 Sequence 202802, A
26	27.6	25.6	26050	4	US-09-949-016-17449 Sequence 17449, A
27	27.6	25.6	98844	3	US-09-791-211-10 Sequence 10, Appl

28	27.6	25.6	143776	4	US-09-949-001-29 Sequence 29, Appl
29	27.6	25.6	144034	4	US-09-949-001-35 Sequence 35, Appl
30	27.4	25.4	483	4	US-09-583-110-2272 Sequence 2272, Ap
31	27.4	25.4	489	4	US-09-107-433-492 Sequence 492, App
32	27.4	25.4	601	4	US-09-949-016-82861 Sequence 82861, A
33	27.4	25.4	957	1	US-08-309-182B-1 Sequence 1, Appl
34	27.4	25.4	1117	4	US-09-552-225A-11 Sequence 11, Appl
35	27.4	25.4	1851	4	US-09-949-016-3036 Sequence 3036, Ap
36	27.4	25.4	2120	3	US-09-149-476-160 Sequence 160, App
37	27.4	25.4	2628	4	US-09-774-528-27 Sequence 27, Appl
38	27.4	25.4	8590	4	US-09-949-016-5562 Sequence 5562, Ap
39	27.4	25.4	10300	4	US-09-949-016-636 Sequence 636, App
40	27.4	25.4	38575	4	US-09-949-016-17304 Sequence 17304, A
41	27.4	25.4	119153	4	US-09-949-016-12378 Sequence 12378, A
42	27.4	25.4	213456	4	US-09-820-007-3 Sequence 3, Appl
43	27.4	25.4	323820	4	US-09-949-016-14139 Sequence 14139, A
44	27.2	25.2	7644	4	US-09-949-016-17610 Sequence 17610, A
45	27	25.0	372	4	US-09-270-767-5510 Sequence 5510, Ap

ALIGNMENTS

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; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549, 872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129, 596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9

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Matches 70; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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DB 54 TGAATGCTCCTACAGACGCTCAAACTTCAGAACATTTATCAATTTCTCTAT 113
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RESULT 2
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; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549, 872B
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
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; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
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; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PLB cDNA
US-09-549-872B-13
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Best Local Similarity 68.6%; Pred. No. 5,6e-08;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
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OY 66 TCTCATCTGCTCTCTGCTGATTTGCATTATGTCGATGCTCT 107
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DB 114 CTTAATATGCTCTTCTGCTGATTCATTCATTCGATGCTCTCT 155
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RESULT 3
US-09-513-999C-10799
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
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; LENGTH: 480
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; ORGANISM: Homo sapiens
US-09-513-999C-10799
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DB 249 TGAATGCTCTAACAAGACGCTCAAACTTCAGAACTTATTCATATTCGTCTCAT 308
OY 66 TCTCATCTGCTCTCTGCTGATTTGCATTATGTCGATGCTCT 107
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DB 309 CTTAATATGCTCTTCTGCTGATTCATTCATTCGATGCTCTCT 350
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RESULT 4
US-09-949-016-1439
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439
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Best Local Similarity 65.7%; Pred. No. 6,7e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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OY 66 TCTCATCTGCTCTCTGCTGATTTGCATTATGTCGATGCTCT 107
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DB 295 CTTAATATGCTCTTCTGCTGATTCATTCATTCGATGCTCTCT 336
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RESULT 5
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; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13181
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181
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Best Local Similarity 65.7%; Pred. No. 1,7e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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OY 66 TCTCATCTGCTCTCTGCTGATTTGCATTATGTCGATGCTCT 107
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DB 12721 CTTAATATGCTCTTCTGCTGATTCATTCATTCGATGCTCTCT 12762
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US-09-124-671-26
; Sequence 26, Application US/09124671A
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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: July 7, 2005, 09:22:55 ; Search time 260.444 Seconds
(without alignments)
2603.465 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications NA.*
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Pred. No. is the number of results predicted by chance a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	108	100.0	135	20	US-10-724-532-5
4	108	100.0	135	20	US-10-724-532-6
5	50.8	47.0	159	15	US-10-371-101-9
6	50.8	47.0	159	15	US-10-371-101-13
7	46	42.6	159	19	US-10-691-412-1

8	46	42.6	525	10	US-09-918-995-4045	Sequence 4045, Ap
9	46	42.6	1635	10	US-09-873-367C-162	Sequence 162, App
10	46	42.6	1635	21	US-10-843-641A-162	Sequence 162, App
11	45	41.7	380	10	US-09-918-995-3950	Sequence 3950, Ap
12	45	41.7	418	10	US-09-918-995-5235	Sequence 5235, Ap
13	44.4	41.1	394	10	US-09-918-995-4217	Sequence 4217, Ap
14	44.4	41.1	487	10	US-09-918-995-5377	Sequence 5377, Ap
15	44.4	40.4	315	20	US-10-815-514-26	Sequence 26, Appl
16	43.6	40.4	315	20	US-10-877-990-26	Sequence 26, Appl
17	43.6	40.4	315	21	US-10-873-554-26	Sequence 26, Appl
18	41.2	38.1	407	10	US-09-918-995-3842	Sequence 3842, Ap
19	38	35.2	492	10	US-09-918-995-17377	Sequence 17377, A
20	32.8	30.4	652	11	US-09-969-034-4348	Sequence 4348, Ap
21	32.8	30.4	1896	21	US-10-723-518-2	Sequence 2, Appl
22	32.8	30.4	2419	10	US-09-814-353-0506	Sequence 20506, A
23	32.8	30.4	3647	17	US-10-172-118-1260	Sequence 1260, Ap
24	32.8	30.4	3647	18	US-10-342-887-1260	Sequence 1260, Ap
25	32.8	30.4	3647	21	US-10-848-755A-148	Sequence 148, App
26	32.8	30.4	3748	9	US-09-925-301-80	Sequence 80, Appl
27	32.8	30.4	3925	20	US-10-723-860-4598	Sequence 4598, Ap
28	32	29.6	6481	15	US-10-037-270-1076	Sequence 1076, Ap
29	32	29.6	6481	17	US-10-117-722-1076	Sequence 1076, Ap
30	32	29.6	10625	9	US-09-727-384-5	Sequence 5, Appl
31	32	29.6	10625	14	US-10-023-219-3	Sequence 3, Appl
32	32	29.6	10625	21	US-10-690-276-3	Sequence 3, Appl
33	31.8	29.4	2180	18	US-10-425-114-557	Sequence 557, App
34	31.8	29.4	2220	20	US-10-425-115-16740	Sequence 16740, A
35	30.4	28.1	613	19	US-10-767-701-25701	Sequence 25701, A
36	30.4	28.1	1938	13	US-10-087-192-740	Sequence 740, App
37	30.4	28.1	2175	9	US-09-994-485-3	Sequence 3, Appl
38	30.4	28.1	2175	9	US-09-832-292-7	Sequence 7, Appl
39	30.2	28.0	639	21	US-10-470-048B-40	Sequence 40, Appl
40	30	27.8	415	9	US-09-864-761-3336	Sequence 3236, Ap
41	30	27.8	1269	19	US-10-767-963-88641	Sequence 1475, Ap
42	29.8	27.6	1137	19	US-10-437-963-88641	Sequence 88641, A
43	29.8	27.6	113306	17	US-10-292-798-1007	Sequence 1007, App
44	29.8	27.6	251199	21	US-10-482-029-205	Sequence 205, App
45	29.6	27.4	605	13	US-10-027-632-238890	Sequence 238890, A

ALIGNMENTS

RESULT 1
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724.532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

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Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 CTGATTCATCTGCTCTGCTGATTTGATTAATCGTCATGCTCTG 108

RESULT 2
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

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US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match 100.0%; Score 108; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 1,4e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

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Best Local Similarity 100.0%; Pred. No. 1,4e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035. US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

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Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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CTTAATATGCTCTTGTGCTGATTTGATTAATCGTCATGCTCTG 155

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Best Local Similarity 69.6%; Pred. No. 2.2e-06;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Qy 62 AAAGCATCTGAGGTTCTGCTGCGCTGAGGCTTCTCTCA 103
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Db 618 AATAGTTCTGAGGTTTGAAGTCTGTTGAGGCAATTCA 577
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RESULT 2
LOCUS OCPHAM 2841 bp mRNA linear MAM 24-JUL-1992
DEFINITION O. cuniculus mRNA for phospholamban.
ACCESSION Y00761
VERSION Y00761.1 GI:1661
KEYWORDS phospholamban.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
REFERENCE 1 (bases 1 to 2841)
AUTHORS Fujii J., Lytton J., Tada M. and MacLennan D.H.
TITLE Rabbit cardiac and slow-twitch muscle express the same
JOURNAL phospholamban gene
MEDLINE FEBS Lett. 227 (1), 51-55 (1988)
PUBMED 88112222
FEATURES
source 2962883
Location/Qualifiers
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Db 332 AGAAGCATGACGATGATCAGATCAGCAGAGACATATCAAGATGAGACAGAAATTGATA 273
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Qy 62 AAAGCATCTGAGGTTCTGCTGCGCTGAGGCTTCTCTCA 103
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Db 272 AATAGTTCTGAGGTTTGAAGTCTGTTGAGGCAATTCA 231
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RESULT 3
LOCUS BD247907 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE Sus sp.
ORGANISM Sus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 159)

AUTHORS Zwaal R., Groenen J. and Bogaert T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV

COMMENT
OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1..159
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Db 95 AATAGTTCTGAGGTTTGAAGTCTGTTGAGGCAATTCA 54
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DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE JP 2002541859-A/13.
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal R., Groenen J. and Bogaert T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV

COMMENT
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG PLB CDNA FH
Key Location/Qualifiers
FT source 1..159
Location/Qualifiers
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ORIGIN
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Best Local Similarity 68.6%; Pred. No. 6e-06;
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	25	32.8	30.4	3647	13	ACN383837	Acn383837 Tumour-ae						
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	42	30	27.8	415	4	AAI34661	Aai34661 Probe #33						
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AC	AAC64967;												
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KW	Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;												
KM	cardiac hypertrophy; heart failure; hypertension; Daxier-White disease;												
KN	Brody's disease; diabetes; se.												
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OS	Sus scrofa.												
PV	GB2349217-A.												
PD	25-OCT-2000.												
XX													
PF	14-APR-2000; 2000GB-00009363.												
XX													
PR	15-APR-1999; 99GB-00008670.												
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PR	01-JUN-1999; 99GB-00012736.												
XX													
PA	(DEVG-) DEVGEN NV.												
PI	Zwaal R, Groenen J, Bogaert T;												
DR	WPI; 2000-658082/64.												

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hyperextension, diabetes, Darter-White disease and Brody's disease
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SQ Sequence 159 BP, 45 A, 41 C, 22 G, 51 T, 0 U, 0 Other;
Query Match 47.0%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.3e-06;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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DB 155 AGAAGCATCAGCATGATCAATCAGCAAGAGCATATTAGATGAGACAGAAATTGATA 96
QY 62 AAAGCATCTGAGGCTTCTGCTGCGCTGAGGCGCTTCTCTCA 103
DB 95 AATAGCTTCTGAGGTTTGTGACGCTCTTGTGAGGCATTTC 54
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ID ADBS3082 standard; DNA, 701 BP.
AC ADBS3082;
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DT 04-DEC-2003 (first entry)
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DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.
XX
KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
PN W02003065993-A2.
XX
PD 14-AUG-2003.
XX
PF 04-FEB-2003; 2003WO-US003482.
XX
XX 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elshof M;
XX
XX WPI; 2003-731472/69.
XX
XX
XX Determining if a compound induces a toxic effect on a tissue or cell, for
XX identifying hepatotoxic compounds, comprises comparing a gene expression
XX profile of a tissue or cell sample to a database of Tox mean and non-Tox
XX mean values.
PS Claim 44; SEQ ID NO 3624; 8749P; English.

XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
SQ Sequence 701 BP, 184 A, 178 C, 141 G, 198 T, 0 U, 0 Other;
Query Match 46.5%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 8.1e-06;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 CAGAGCATGACGATATGCAATTCAGCAGAGCGCAGATGAGATCAGCAAAAGCAT 60
DB 329 CAGAGCATGACGATATGCAATTCAGCAGAGCATATCAAGATGAGACAGAAATTGAT 270
QY 61 GAAGCATCTGAGGCTTCTGCTGCGCTGAGGCGCTTCTCTCA 103
DB 269 AAAGGCTTCTGAGGTTTGTGACCGCTTGTGAGGCGATTTC 227
RESULT 3
ADR97285/C
ID ADR97285 standard; DNA, 159 BP.
AC ADR97285;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human phospholamban polymorphism fragment DNA.
XX
KW ds; human; phospholamban; polymorphism; cardiovascular disease.
XX
OS Homo sapiens.
XX
PN US2004191802-A1.
XX
PD 30-SEP-2004.
XX
PF 22-OCT-2003; 2003US-00691412.
XX
PR 22-OCT-2002; 2002US-0420295P.
XX
PA (KRANV/) KRANTAS E G.
XX (HAGH/) HAGHIGHI K.
XX
PI Kranias EG, Haghighi K;
XX
XX WPI; 2004-689841/67.
XX
XX
XX Phospholamban polymorphism assessment in individual, for determining risk
XX for developing cardiovascular disease, by comparing analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence.
PS Claim 15; SEQ ID NO 1, 159P; English.
XX
XX
XX The invention relates to a method of phospholamban polymorphism
XX assessment in an individual which comprises comparing the analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence to determine whether the individual carries a
XX phospholamban polymorphism. The methods and phospholamban polymorphism
XX fragment are useful for determining if an individual is at risk for

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 / Search time 1353.33 seconds
(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-4

Perfect score: 108

Sequence: 1 caggagcatgacatcatgc.....tgaagcctctctcatcatgc 108

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:

1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50.8	47.0	381	5	BX669692 BX669692
2	50.8	47.0	702	5	BX922974 BX922974
3	50.8	47.0	724	5	BX674983 BX674983
4	50.8	47.0	740	5	BX924154 BX924154
5	50.8	47.0	758	5	BX923697 BX923697
6	50.8	47.0	811	7	CK449263 CK449263
7	50.2	46.5	179	2	BE113353 BE113353
8	50.2	46.5	377	2	BF547332 BF547332
9	50.2	46.5	417	1	AI322542 AI322542
10	50.2	46.5	439	1	BE115006 BE115006
11	50.2	46.5	449	2	BE098177 BE098177
12	50.2	46.5	449	2	BE098177 BE098177
13	50.2	46.5	451	4	BI288911 BI288911
14	50.2	46.5	454	4	BE099930 BE099930
15	50.2	46.5	476	2	BF525258 BF525258
16	50.2	46.5	480	7	CR471116 CR471116
17	50.2	46.5	487	4	BG379827 BG379827
18	50.2	46.5	498	1	AI603160 AI603160
19	50.2	46.5	511	1	BF395370 BF395370
20	50.2	46.5	513	4	BI296789 BI296789
21	50.2	46.5	518	2	BE112568 BE112568
22	50.2	46.5	527	2	BF395607 BF395607
23	50.2	46.5	528	2	BF395670 BF395670
24	50.2	46.5	540	2	BF395398 BF395398

25	50.2	46.5	575	4	BI290034 BI290034
26	50.2	46.5	589	2	BF525010 BF525010
27	50.2	46.5	608	1	AI103929 AI103929
28	50.2	46.5	699	7	CK358482 CK358482
29	50.2	46.5	710	7	CK359590 CK359590
30	50.2	46.5	718	7	CK358464 CK358464
31	50.2	46.5	719	7	CK356296 CK356296
32	50.2	46.5	731	7	CK357243 CK357243
33	50.2	46.5	737	7	CK357232 CK357232
34	50.2	46.5	738	7	CK355359 CK355359
35	50.2	46.5	744	7	CK357123 CK357123
36	50.2	46.5	744	7	CK356439 CK356439
37	50.2	46.5	744	7	CK357747 CK357747
38	50.2	46.5	745	7	CK355314 CK355314
39	50.2	46.5	745	7	CK356371 CK356371
40	50.2	46.5	748	7	CK359219 CK359219
41	50.2	46.5	754	7	CK355445 CK355445
42	50.2	46.5	758	7	CK355453 CK355453
43	50.2	46.5	758	7	CK357746 CK357746
44	50.2	46.5	762	7	CK359188 CK359188
45	50.2	46.5	764	7	CK357447 CK357447

ALIGNMENTS

RESULT 1	BX669692/c	381 bp	mRNA	linear	EST 07-MAY-2004
LOCUS	BX669692				
DEFINITION	BX669692 Sus scrofa library (scac) Sus scrofa cDNA clone				
ACCESSION	scac00281.c.02				
VERSION	BX669692				
KEYWORDS	BX669692.1 GI:37979481				
SOURCE	EST				
ORGANISM	Sus scrofa (pig)				
REFERENCE	Sus scrofa				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 381)				
TITLE	Soares, M., Ronaldo, F., and Hately, F., A Pig Normalised Multi-Tissue cDNA Library				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Tosser-Klopp G				
	Genetique Animale				
	Institut National de la Recherche Agronomique				
	Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE				
	Tel: 33 (0) 5.61.28.51.14				
	Fax: 33 (0) 5.61.28.53.08				
	Email: tosser@toulouse.inra.fr				
	Sequence cleaned of vector, adaptor and repetitions. Contact us at eigenasupport@inra.fr to obtain the chromatogram of this sequence.				
FEATURES	Plate: 0028				
source	row: c column: 2.				
	Location/Qualifiers				
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	/mol_type="mRNA"				
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	/clone="scac00281.c.02"				
	/tissue_type="mixed"				
	/clone_lib="Sus Scrofa library (scac)"				
	/note="Vector: pTRIP-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"				
ORIGIN					
Query Match	47.0%; Score 50.8; DB 5; Length 381;				

Best Local Similarity 68.6%; Pred. No. 0.00012;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 2 AGGAGCATGACGATTAATGCAATTCAGCGAGGAGGATGAGAAATCAGCAAAAGCAATG 61
Db 183 AGAAGCATCAGCATGATGCAAAATCAGCAAGGCAATTAATTAAGATGACAGAAATTGATA 124
OY 62 AAAGCATTCGAGGTTCTGCGCTGCGCTGAGGCTTCTCA 103
Db 123 AATAGTTCTGAAGGTTTGAAGCTGCTTTGAGGCAATTCA 82

RESULT 2
BX922974/c 702 bp mRNA linear EST 07-MAY-2004
LOCUS BX922974 Sus Scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan0013d.f.14 5prim, mRNA sequence.

ACCESSION BX922974
VERSION BX922974.1 GI:41139822
KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

REFERENCE Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 702)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,

Soares, M., Bonaldo, F. and Hately, F.

A Pig Normalised Multi-Tissue cDNA Library

Unpublished (2003)

CONTACT: Tosser-Klopp G

Genetique Animale

Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0013 row: j column: 14.

Location/Qualifiers

FEATURES

source

1..702

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scan0013d.f.14"

/tissue_type="mixed"

/dev_stage="from embryos to adults"

/clone_lib="Sus Scrofa library (scan)"

/note="Tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN

Query Match 47.0%; Score 50.8; DB 5; Length 702;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 2 AGGAGCATGACGATTAATGCAATTCAGCGAGGAGGATGAGAAATCAGCAAAAGCAATG 61
Db 317 AGAAGCATCAGCATGATGCAAAATCAGCAAGGCAATTAATTAAGATGACAGAAATTGATA 258

OY 62 AAAGCATTCGAGGTTCTGCGCTGCGCTGAGGCTTCTCA 103
Db 257 AATAGTTCTGAAGGTTTGAAGCTGCTTTGAGGCAATTCA 216

RESULT 3

BX674983/c 724 bp mRNA linear EST 07-MAY-2004
LOCUS BX674983 Sus Scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan00391.h.23 5prim, mRNA sequence.

ACCESSION BX674983

VERSION BX674983.1 GI:38008935

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

REFERENCE Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 724)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,

Soares, M., Bonaldo, F. and Hately, F.

A Pig Normalised Multi-Tissue cDNA Library

Unpublished (2003)

CONTACT: Tosser-Klopp G

Genetique Animale

Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0039 row: h column: 23.

Location/Qualifiers

FEATURES

source

1..724

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scan00391.h.23"

/tissue_type="mixed"

/clone_lib="Sus Scrofa library (scan)"

/note="Vector: pT7SD-pec vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 47.0%; Score 50.8; DB 5; Length 724;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 2 AGGAGCATGACGATTAATGCAATTCAGCGAGGAGGATGAGAAATCAGCAAAAGCAATG 61
Db 338 AGAAGCATCAGCATGATGCAAAATCAGCAAGGCAATTAATTAAGATGACAGAAATTGATA 279

OY 62 AAAGCATTCGAGGTTCTGCGCTGCGCTGAGGCTTCTCA 103
Db 278 AATAGTTCTGAAGGTTTGAAGCTGCTTTGAGGCAATTCA 237

RESULT 4

BX924154/c 740 bp mRNA linear EST 07-MAY-2004
LOCUS BX924154 Sus Scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan0011d.f.23 5prim, mRNA sequence.

ACCESSION BX924154

VERSION BX924154.1 GI:41141002

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

REFERENCE Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 740)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.


```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HUMANIZED PIG
; OTHER INFORMATION: P1B cDNA
US-09-549-872B-13

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Query Match          47.0%; Score 50.8; DB 4; Length 159;
Best Local Similarity 68.6%; Pred. No. 5.6e-08;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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DB 155 AGAAGCATCAGATGATGCAATTCAGCAAGAGGCGATTAATGAGATGAGACAGAAATTGATA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGCCCTGAGCCCTTCTCTCA 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 95 AATAGATTCTGAAAGGTTTGGACGTGCTTGTGGAGGCATTTC 54
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RESULT 3

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US-09-513-999C-10799/C
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 10799
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799

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Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 350 AGAAGCATCAGATGATGCAATTCAGATCAGCAAGAGCAATTAATGAGATGAGACAGAAATTGATA 291
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QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGCCCTGAGCCCTTCTCTCA 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 290 AATAGATTCTGAGCTTTTGAAGTGTGCTGTTGAGGCATTTC 249
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RESULT 4
US-09-949-016-1439/C
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439

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Query Match          42.6%; Score 46; DB 4; Length 1635;
Best Local Similarity 65.7%; Pred. No. 6.7e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 2 AGAGCATGACGATTAATGCAATTCAGCAGAGGCGATGAGATCAGACAAAGCAATG 61
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DB 336 AGAAGCATCAGATGATGCAATTCAGATCAGCAAGAGCAATTAATGAGATGAGACAGAAATTGATA 277
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QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGCCCTGAGCCCTTCTCTCA 103
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DB 276 AATAGATTCTGAGCTTTTGAAGTGTGCTTGTGGAGGCATTTC 235
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RESULT 5

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US-09-949-016-13181/C
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13181
; LENGTH: 16062
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181

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Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGCCCTGAGCCCTTCTCTCA 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12702 AATAGATTCTGAGCTTTTGAAGTGTGCTTGTGGAGGCATTTC 12661
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RESULT 6
US-09-124-671-26/C
; Sequence 26, Application US/09124671A

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Db 48 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 1

RESULT 2
US-10-724-532-4
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Query Match 100.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGAGCATGACGATTAATGCAATCAGCAGGAGCAGATGAGAAATCAGACAAAGCAAT 60
Db 1 CAGAGCATGACGATTAATGCAATCAGCAGGAGCAGATGAGAAATCAGACAAAGCAAT 60

Qy 61 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 108
Db 61 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 108

RESULT 3
US-10-724-532-5/c
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match 100.0%; Score 108; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGAGCATGACGATTAATGCAATCAGCAGGAGCAGATGAGAAATCAGACAAAGCAAT 60
Db 120 CAGAGCATGACGATTAATGCAATCAGCAGGAGCAGATGAGAAATCAGACAAAGCAAT 61

Qy 61 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 108
Db 60 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 13

RESULT 4

US-10-724-532-6
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

Query Match 100.0%; Score 108; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 CAGAGCATGACGATTAATGCAATCAGCAGGAGCAGATGAGAAATCAGACAAAGCAAT 75

Qy 61 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 108
Db 76 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAAT 123

RESULT 5
US-10-371-101-9/c
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

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Best Local Similarity 68.6%; Pred. No. 3.8e-07;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 2 AGAGCATGACGATTAATGCAATCAGCAGGAGCAGATGAGAAATCAGACAAAGCAATG 61
Db 155 AGAGCATGACGATTAATGCAATCAGCAGGAGCAGATTAAGATGAGACAGAAATTTGATA 96

Qy 62 AAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCA 103
Db 95 AATAGTTCTGAGGTTTGAAGTGCTGCTTGTGAGGCATTTCGA 54

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Run on: July 7, 2005, 09:02:25 ; Search time 1249.17 Seconds
(without alignments)
5236.654 Million cell updates/sec

Title: US-10-724-532-5

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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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7: gb_ph : *
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9: gb_pr : *
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11: gb_str : *
12: gb_sy : *
13: gb_un : *
14: gb_vi : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.4	38.8	858	4	RABPHLAM2
2	52.4	38.8	2841	4	OCPHLAM
3	50.8	37.6	159	6	BD247907
4	50.8	37.6	159	6	BD247911
5	50.8	37.6	159	6	AR302003
6	50.8	37.6	159	6	AR302007
7	50.8	37.6	159	6	AX040487
8	50.8	37.6	159	6	AX040491
9	50.8	37.6	737	4	SSPLB
10	50.2	37.2	159	10	S95853
11	50.2	37.2	386	10	S95849
12	50.2	37.2	701	10	RNPPLAMB
13	50.2	37.2	1786	10	RATPHOLA02
14	50.2	37.2	223728	2	AC097906
15	50.2	37.2	231910	5	AC128365
16	47.6	35.3	130240	5	BX276081
17	47.4	35.1	133901	5	BX537355
18	47	34.8	648	10	BC061097
19	47	34.8	940	10	S46792

20	47	34.8	79895	2	AC100317	AC100317 Mus muscu
21	47	34.8	177018	2	AC099716	AC099716 Mus muscu
22	46.6	34.5	3312	5	CHKPLB	M59039 Chicken car
23	46.6	34.5	3423	5	CHKPLB2	M59038 Chicken pho
24	46	34.1	306	6	CQ447405	CQ447405 Sequence
25	46	34.1	323	9	HDMPLAM	M60411 Human phosp
26	46	34.1	480	6	AX894936	AX894936 Sequence
27	46	34.1	480	6	BD030469	BD030469 Sequence
28	46	34.1	980	9	HSP18G2	AF177764 Homo sapi
29	46	34.1	1635	6	CQ718671	CQ718671 Sequence
30	46	34.1	1635	6	AX329653	AX329653 Sequence
31	46	34.1	1635	9	HDMPLAM	M63603 Human phosp
32	46	34.1	1691	9	BC005269	BC005269 Homo sapi
33	46	34.1	60797	2	AL355356	AL355356 Homo sapi
34	46	34.1	66092	2	AL136974	AL136974 Homo sapi
35	46	34.1	150290	4	HS050914	Z99496 Human DNA s
36	44.4	32.9	314	4	AY514751	AY514751 Canis fam
37	44.4	32.9	832	4	DOGPHL	M16012 Canine card
38	44.4	32.9	832	4	DOGPHL2	M16012 Canine card
39	44.4	32.9	2614	4	CEPHLX	M35393 Dog phospha
40	44.2	32.7	315	6	AR121629	AR121629 Sequence
41	36.2	26.8	147419	9	HS738P11	AL031736 Human DNA
42	35.6	26.4	184450	2	AC116417	AC116417 Mus muscu
43	35.2	26.1	209299	5	AC145916	AC145916 Gallus ga
44	35	25.9	5702	6	CQ719769	CQ719769 Sequence
45	35	25.9	6481	6	AR339585	AR339585 Sequence

ALIGNMENTS

RESULT 1	RABPHLAM2	858 bp	DNA	linear	MAM 27-APR-1993
LOCUS	RABPHLAM2				
DEFINITION	Rabbit phospholamban gene, partial exon 2.				
ACCESSION	M63601.1	GI:165636			
VERSION	M63601.1	GI:165636			
KEYWORDS	phospholamban.				
SEGMENT	2 of 3				
SOURCE	Oryctolagus cuniculus (rabbit)				
ORGANISM	Oryctolagus cuniculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
AUTHORS	Fujii, J., Zarain-Herzberg, A., Willard, H.F., Tada, M. and MacLennan, D.H.				
TITLE	Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6				
JOURNAL	J. Biol. Chem. 266 (18), 11669-11675 (1991)				
MEDLINE	91268032				
PUBMED	1828805				
COMMENT	Original source text: Rabbit DNA.				
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source	1..858				
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	/feature_1lb="Rabbit genomic"				
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	428..858				
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	/number=2				
	524..682				
	/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"				
	/codon_start=1				
	/product="phospholamban"				
	/protein_id="AA31445.1"				
	/db_xref="GI:165639"				
	/translation="MERKQYVTRSAIRRASTIEMPDQARONLQNLINFCULILCLLL				
	ICIIIVML"				

ORIGIN

[illegible]

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OM nucleic - nucleic search, using bw model

Run on: July 7, 2005, 09:02:25 ; Search time 256.389 Seconds
(without alignments)
3117.004 Million cell updates/sec

Title: US-10-724-532-5

Perfect score: 135
Sequence: 1 gagagaagcctatgcacga.....tccctgcgagagagagag 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: N_Geneseq_16Dec04:*
2: geneeqn1980a:*
3: geneeqn1990a:*
4: geneeqn2000a:*
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6: geneeqn2002a:*
7: geneeqn2003a:*
8: geneeqn2004a:*
9: geneeqn2005a:*
10: geneeqn2006a:*
11: geneeqn2007a:*
12: geneeqn2008a:*
13: geneeqn2009a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	50.8	37.6	159 3	AAC64967 Pig phosp
2	50.2	37.2	701 10	ADB53082 Primary r
3	46	34.1	159 13	ADR97285
4	46	34.1	306 6	ABN22344
5	46	34.1	480 3	AAC06724 Human ORF
6	46	34.1	525 9	ACH16853 Human sec
7	46	34.1	1635 6	ABL61825 Human ade
8	46	34.1	1635 12	ADN04087 Antipocrt
9	46	34.1	1712 12	ADP21384 Gene PLN
10	45	33.3	380 9	ACH16738 Human adu
11	45	33.3	418 9	ACH18023 Human adu
12	44.4	32.9	394 9	ACH17005 Human adu
13	44.4	32.9	487 9	ACH18165 Human adu
14	44.2	32.7	312 3	AAZ50498 KDEL rece
15	41.2	30.5	407 9	ACH16630 Human adu
16	38	28.1	492 6	ACH30165 Human tes
17	36.2	147419	6	ABK83574 Human CDV
18	35	25.9	6481 4	AA159183 Human pol
19	35	25.9	6481 5	ADQ99406 DNA encod
20	35	25.9	6481 9	ADB49166 Novel hum

C 21	35	25.9	6536	3	AAC75801
C 22	35	25.9	10625	5	AAC85836
C 23	35	25.9	10625	6	AA141031
C 24	33.6	24.9	652	6	ABO60653
C 25	33.6	24.9	1896	12	ADP07907
C 26	33.6	24.9	2419	5	AD162294
C 27	33.6	24.9	2422	10	ADC37617
C 28	33.6	24.9	3647	6	ABK83658
C 29	33.6	24.9	3647	10	ADP81412
C 30	33.6	24.9	3647	13	ADR25399
C 31	33.6	24.9	3647	13	ACN38837
C 32	33.6	24.9	3708	2	AAZ77530
C 33	33.6	24.9	3748	3	AAZ77530
C 34	33.6	24.9	3925	12	ADQ21778
C 35	32.6	24.1	11306	10	ADC86554
C 36	31.4	23.3	1938	11	ACN44341
C 37	31.4	23.3	2175	2	AAZ24806
C 38	31.2	23.1	473	13	ADQ79072
C 39	31.2	23.1	2229	6	ABK74380
C 40	30.8	22.8	415	4	AA113308
C 41	30.8	22.8	415	4	ABA55007
C 42	30.8	22.8	415	4	AA134661
C 43	30.8	22.8	415	4	ABA44562
C 44	30.8	22.8	415	4	ABA24770
C 45	30.8	22.8	415	4	AAK28730

ALIGNMENTS

RESULT 1	AAC64967	standard; cDNA; 159 BP.
ID	AAC64967	
XX	XX	
AC	AAC64967;	
XX	XX	
DT	09-FEB-2001 (first entry)	
XX	XX	
DE	Pig phospholamban cDNA.	
XX	XX	
KW	Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;	
KW	cardiac hypertrophy; heart failure; hypertension; Darter-white disease;	
KW	Brody's disease; diabetes; ss.	
XX	XX	
OS	Sus scrofa.	
XX	XX	
PN	GB2349217-A.	
XX	XX	
PD	25-OCT-2000.	
XX	XX	
PF	14-APR-2000; 2000GB-00009363.	
XX	XX	
PR	15-APR-1999; 99GB-00008670.	
PR	15-APR-1999; 99US-0129596P.	
PR	01-JUN-1999; 99GB-00012736.	
XX	XX	
PA	(DEVC-) DEVCEN NV.	
XX	XX	
DR	WPI; 2000-658082/64.	
PT	Identifying modulators of sarco/endoplasmic reticulum calcium ATPase.	
PT	useful potentially for treating disorders of calcium homeostasis, e.g.	
PT	cardiac hypertrophy.	
XX	XX	
PS	Disclosure; Fig 11; 108bp; English.	
CC	The present invention is concerned with methods of using C. elegans to	
CC	identify compounds which are capable of up- and down-regulating the	
CC	activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This	
CC	protein is involved in cell signalling, and elevated levels affect	
CC	cellular processes such as contraction, secretion and cell cycling. The	

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hyperextension, diabetes, Darier-White disease and Brody's disease
XX

SO Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;

Query Match 37.6%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 6.9e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 18 TGAAGAGAGCGCTCAGGCGCAGACCTCCAGAACTTTCATGCTTTTGTCTGAT 77
Db 54 TGAATGCTCCACAGACGCTCAAAACCTTCAGAACTTTCATGCTTTTGTCTGAT 113

Qy 78 TCTCATCTGCTCCTCGCTGATTTGATTCATTCATGCTCTCT 119
Db 114 CTTATATGCTCTTCTGCTGATTCATTCATTCATGCTCTCT 155

RESULT 2
ID ADB53082 standard; DNA; 701 BP.

XX ADB53082;

DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.

XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.

OS Rattus norvegicus.

XX WO2003065993-A2.

PD 14-AUG-2003.

PF 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.

PR 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373601P.

PR 12-APR-2002; 2002US-0373602P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-MAY-2002; 2002US-0378655P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elshoff M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
XX identifying hepatotoxic compounds, comprises comparing a gene expression
XX profile of a tissue or cell sample to a database of tox mean and non-tox
XX mean values.

PS Claim 44; SEQ ID NO 3624; 874pp; English.

XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the tox mean and non-tox mean value.

CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

Qy Sequence 701 BP; 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;

Query Match 37.2%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 1.7e-05;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 18 TGAAGAGAGCGCTCAGGCGCAGACCTCCAGAACTTTCATGCTTTTGTCTGAT 77
Db 227 TGAATGCCCCAGAGCGGCTCAGAACTTCAGAACTTTCATGCTTTTGTCTGAT 286

Qy 78 TCTCATCTGCTCCTCGCTGATTTGATTCATTCATGCTCTCTG 120
Db 287 CTTGATATGCTCTGCTGATTCATTCATTCATGCTCTCTG 329

RESULT 3
ID ADR97285 standard; DNA; 159 BP.

XX ADR97285;

DT 16-DEC-2004 (first entry)

DE Human phospholamban polymorphism fragment DNA.

XX ds; human; phospholamban; polymorphism; cardiovascular disease.

XX Homo sapiens.

OS US2004191802-A1.

PD 30-SEP-2004.

PF 22-OCT-2003; 2003US-00691412.

XX 22-OCT-2002; 2002US-0420295P.

PR (KRAN/) KRANIAS E. G.

PA (HAGH/) HAGHIGHT K.

XX Kranias EG, Haghighi K;

PI WPI; 2004-689841/67.

XX Phospholamban polymorphism assessment in individual, for determining risk

XX for developing cardiovascular disease, by comparing analysis of the

XX nucleotide fragment with a predetermined phospholamban nucleotide

XX fragment sequence.

XX Claim 15; SEQ ID NO 1; 15pp; English.

XX The invention relates to a method of phospholamban polymorphism

XX assessment in an individual which comprises comparing the analysis of the

XX nucleotide fragment with a predetermined phospholamban nucleotide

XX fragment sequence to determine whether the individual carries a

XX phospholamban polymorphism. The methods and phospholamban polymorphism

XX fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1691.67 Seconds
(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-5
Perfect score: 135
Sequence: 1 gagagaagaactatcatcatga.....tccctgcgcgagagagagag 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_esc2:*
3: gb_hnc:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50.8	37.6	381	5	BX669692 BX669692
2	50.8	37.6	702	5	BX922974 BX922974
3	50.8	37.6	724	5	BX674983 BX674983
4	50.8	37.6	740	5	BX924154 BX924154
5	50.8	37.6	758	5	BX923697 BX923697
6	50.8	37.6	811	7	CK449263 892817 MA
7	50.2	37.2	179	2	BE113353 UI-R-BJ1-
8	50.2	37.2	377	2	BF547322 UI-R-C2P-
9	50.2	37.2	417	1	AI322542 mh89506.Y
10	50.2	37.2	439	2	BE115006 UI-R-BJ1-
11	50.2	37.2	449	2	BF394968 UI-R-CMO-
12	50.2	37.2	449	2	BE098177 UI-R-BJ1-
13	50.2	37.2	451	4	BE128891 UI-R-C508
14	50.2	37.2	454	2	BE099930 UI-R-BJ1-
15	50.2	37.2	476	2	BF525258 UI-R-ACO-
16	50.2	37.2	480	7	CR471116 CR471116
17	50.2	37.2	487	4	BC379827 UI-R-CSO-
18	50.2	37.2	498	1	AI603160 UI-R-AEO-
19	50.2	37.2	511	4	BF395370 UI-R-CMO-
20	50.2	37.2	513	4	BI296789 UI-R-DKO-
21	50.2	37.2	518	2	BE112568 UI-R-BJ1-
22	50.2	37.2	527	2	BF395607 UI-R-CMO-
23	50.2	37.2	528	2	BF395670 UI-R-CMO-
24	50.2	37.2	540	2	BF395398 UI-R-CMO-

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	26	50.2	37.2	589	2	BF525010 UI-R-AEO-
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	29	50.2	37.2	710	7	CK359590 AGENCOURT
	30	50.2	37.2	719	7	CK358464 AGENCOURT
	31	50.2	37.2	719	7	CK356296 AGENCOURT
	32	50.2	37.2	731	7	CK357243 AGENCOURT
	33	50.2	37.2	737	7	CK357232 AGENCOURT
	34	50.2	37.2	738	7	CK355359 AGENCOURT
	35	50.2	37.2	738	7	CK357123 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS BX669692 381 bp mRNA linear EST 07-MAY-2004
DEFINITION BX669692 Sus scrofa library (scac) Sus scrofa cDNA clone
ACCESION scac00281.c.02 5prim, mRNA sequence.
VERSION BX669692
KEYWORDS BX669692.1 GI:37979481
SOURCE EST.
ORGANISM Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
Auteurs Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F., and Hately, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequences cleaned of vector, adaptor and repetitions. Contact us
at sigena@port@journ.inra.fr to obtain the chromatogram of this
sequence.

FEATURES
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Location/Qualifiers
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/clone="scac00281.c.02"
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/clone_lib="Sus Scrofa library (scac)"
/note="Vector: pT73d-pac vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN
Query Match 37.6%; Score 50.8; DB 5; Length 381;

AUTHORS Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 77.2222 Seconds
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2860.541 Million cell updates/sec

Title: US-10-724-532-5

Perfect score: 135

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	46	34.1	1480	US-09-513-999C-10799	Sequence 10799, A
4	46	34.1	1635	US-09-949-016-1439	Sequence 1439, Ap
5	46	34.1	16062	US-09-949-016-13181	Sequence 13181, A
6	44.2	32.7	315	US-09-124-671-26	Sequence 26, Appl
7	35	25.9	6481	US-09-620-312D-1076	Sequence 1076, Ap
8	31.4	23.3	2175	US-08-914-999-3	Sequence 3, Appl
9	30.6	22.7	1917	US-09-902-540-3588	Sequence 3588, Ap
10	30.6	22.7	19394	US-09-902-540-1172	Sequence 1172, Ap
11	30.2	22.4	65424	US-09-949-016-12426	Sequence 12426, A
12	30.2	22.4	74353	US-09-949-016-15336	Sequence 15336, A
13	29.6	21.9	957	US-08-309-182B-1	Sequence 1, Appl
14	29.6	21.9	8590	US-09-949-016-5562	Sequence 5562, Ap
15	29.6	21.9	10300	US-09-949-016-636	Sequence 636, App
16	29.6	21.9	38575	US-09-949-016-123704	Sequence 123704, A
17	29.6	21.9	119155	US-09-949-016-14880	Sequence 14880, A
18	29.2	21.6	1095	US-09-252-991A-14880	Sequence 14880, A
19	29.2	21.6	1317	US-09-252-991A-14748	Sequence 14748, A
20	29.2	21.6	2622	US-09-513-999C-15001	Sequence 15001, A
21	29	21.5	601	US-09-513-999C-1161	Sequence 1161, Ap
22	29	21.5	474	US-09-949-016-202802	Sequence 202802, A
23	29	21.5	1123	US-09-188-930-28	Sequence 28, Appl
24	29	21.5	1123	US-09-188-930-203	Sequence 203, Appl
25	29	21.5	1123	US-09-312-283C-28	Sequence 28, Appl
26	29	21.5	1123	US-09-312-283C-203	Sequence 203, App
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28	28.8	21.3	879	US-09-489-039A-5041	Sequence 5041, Ap
29	28.6	21.2	601	US-09-949-016-200644	Sequence 200644, A
30	28.6	21.2	601	US-09-949-016-200790	Sequence 200790, A
31	28.6	21.2	46343	US-09-949-016-16824	Sequence 16824, A
32	28.6	21.2	152582	US-09-949-016-12086	Sequence 12086, A
33	28.6	21.2	152583	US-09-949-016-17390	Sequence 17390, A
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36	28.6	21.2	1664976	US-09-692-570-1	Sequence 1, Appl
37	28.4	21.0	1855	US-09-949-016-1929	Sequence 1929, Ap
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39	28.2	20.9	568	US-08-956-171E-999	Sequence 999, App
40	28.2	20.9	568	US-08-781-986A-999	Sequence 999, App
41	28.2	20.9	603	US-08-816-346-5	Sequence 5, Appl
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43	28.2	20.9	1851	US-09-949-016-3036	Sequence 3036, Ap
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ALIGNMENTS

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; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549, 872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129, 596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
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Best Local Similarity 68.6%; Pred. No. 1.2e-07;
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; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549, 872B
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;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: GB 9908670.4
;; PRIOR FILING DATE: 1999-04-15
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;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: GB 9912736.7
;; PRIOR FILING DATE: 1999-06-01
;; NUMBER OF SEQ ID NOS: 39
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;; LENGTH: 159
;; TYPE: DNA
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;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
;; OTHER INFORMATION: PLB CDNA
US-09-549-872B-13

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QY 78 TCTCATCTGCTCCTGCTGATTTGATTCATTCATGCTCTCT 119
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;; Sequence 10799, Application US/09513999C
;; Patent No. 6783961
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Duclet, A.
;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;; FILE REFERENCE: 59, US2, REG
;; CURRENT APPLICATION NUMBER: US/09/513,999C
;; CURRENT FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/122,487
;; PRIOR FILING DATE: 1999-02-26
;; NUMBER OF SEQ ID NOS: 36681
;; SOFTWARE: Patent.pm
;; SEQ ID NO 10799
;; LENGTH: 480
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-513-999C-10799

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RESULT 4
US-09-949-016-1439
;; Sequence 1439, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1439
;; LENGTH: 1635
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-1439

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;; Sequence 13181, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13181
;; LENGTH: 16062
;; TYPE: DNA
;; ORGANISM: Human
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RESULT 6
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	108	80.0	108	20	US-10-724-532-4
5	50.8	37.6	159	15	US-10-371-101-9
6	50.8	37.6	159	15	US-10-371-101-13
7	46	34.1	159	19	US-10-691-412-1

8	46	34.1	525	10	US-09-918-995-4045	Sequence 4045, Ap
9	46	34.1	1635	10	US-09-873-367C-162	Sequence 162, App
10	46	34.1	1635	21	US-10-843-641A-162	Sequence 162, App
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12	45	33.3	418	10	US-09-918-995-5235	Sequence 5235, Ap
13	45	32.9	394	10	US-09-918-995-4217	Sequence 4217, Ap
14	44.4	32.9	487	10	US-09-918-995-5377	Sequence 5377, Ap
15	44.4	32.7	315	20	US-10-815-514-26	Sequence 26, Appl
16	44.2	32.7	315	20	US-10-877-910-26	Sequence 26, Appl
17	44.2	32.7	315	21	US-10-873-554-26	Sequence 26, Appl
18	41.2	30.5	407	10	US-09-918-995-3842	Sequence 3842, Ap
19	38	28.1	492	10	US-09-918-995-17377	Sequence 17377, A
20	35	25.9	6481	15	US-10-037-270-1076	Sequence 1076, Ap
21	35	25.9	6481	17	US-10-117-722-1076	Sequence 1076, Ap
22	35	25.9	10625	9	US-09-727-384-5	Sequence 5, Appl
23	35	25.9	10625	14	US-10-023-219-3	Sequence 3, Appl
24	35	25.9	10625	21	US-10-600-276-3	Sequence 3, Appl
25	33.6	24.9	652	11	US-09-969-034-4348	Sequence 4348, Ap
26	33.6	24.9	1896	21	US-10-723-518-2	Sequence 2, Appl
27	33.6	24.9	2180	18	US-10-425-114-557	Sequence 557, App
28	33.6	24.9	2220	20	US-10-425-115-167740	Sequence 167740, A
29	33.6	24.9	2419	10	US-09-814-353-20506	Sequence 20506, A
30	33.6	24.9	3647	17	US-10-172-118-1260	Sequence 1260, Ap
31	33.6	24.9	3647	18	US-10-342-867-1260	Sequence 1260, Ap
32	33.6	24.9	3647	21	US-10-848-755A-148	Sequence 148, App
33	33.6	24.9	3748	9	US-09-925-301-80	Sequence 80, Appl
34	33.6	24.9	3925	20	US-10-723-860-4598	Sequence 4598, Ap
35	32.6	24.1	113306	17	US-10-292-798-1007	Sequence 1007, Ap
36	32.2	22.9	613	19	US-10-767-701-25701	Sequence 25701, A
37	31.4	23.3	1938	13	US-10-087-192-740	Sequence 740, App
38	31.4	23.3	2175	9	US-09-994-485-3	Sequence 3, Appl
39	31.4	23.3	2175	9	US-09-832-292-7	Sequence 7, Appl
40	31.2	23.1	1137	19	US-10-437-963-88641	Sequence 88641, A
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42	30.8	22.8	415	9	US-09-864-761-3236	Sequence 3236, Ap
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45	30.6	22.7	1878	17	US-10-369-493-43089	Sequence 43089, A

ALIGNMENTS

RESULT 1
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; TITLE OF INVENTION: Reticulum
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724, 532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

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Best Local Similarity 100.0%; Pred. No. 7.7e-36;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ATTCCTTTTGTGATTCATCTATCGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 120
Oy 121 CTCGAGAGAGAGAG 135
Db 121 CTCGAGAGAGAGAG 135

RESULT 2
US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; TITLE OF INVENTION: Reticulum
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

Query Match 100.0%; Score 135; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 7.7e-36;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GAGGAAAGCTTATTCATGAGAGAGGCTTCAGGCGCAGAGAACTTCAGAAATGCTTTC 60
Db 135 GAGGAAAGCTTATTCATGAGAGAGGCTTCAGGCGCAGAGAACTTCAGAAATGCTTTC 76
Oy 61 ATTCCTTTTGTGATTCATCTATCGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 120
Db 75 ATTCCTTTTGTGATTCATCTATCGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 16
Oy 121 CTCGAGAGAGAGAG 135
Db 15 CTCGAGAGAGAGAG 1

RESULT 3
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; TITLE OF INVENTION: Reticulum
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Query Match 80.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 13 ATGCATGAGAGAGGCTTCAGGCGCAGAGAACTTCAGAAATGCTTTCATTTGTTGT 72

Db 1 ATGCATGAGAGAGGCTTCAGGCGCAGAGAACTTCAGAAATGCTTTCATTTGTTGT 60
Oy 73 CTGATTCATCTGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 120
Db 61 CTGATTCATCTGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 108

RESULT 4
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; TITLE OF INVENTION: Reticulum
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Query Match 80.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 13 ATGCATGAGAGAGGCTTCAGGCGCAGAGAACTTCAGAAATGCTTTCATTTGTTGT 72
Db 108 ATGCATGAGAGAGGCTTCAGGCGCAGAGAACTTCAGAAATGCTTTCATTTGTTGT 49
Oy 73 CTGATTCATCTGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 120
Db 48 CTGATTCATCTGCTCTGCTGATTTGCAATTAATGTCATGCTCTG 1

RESULT 5
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Query Match 37.6%; Score 50.8; DB 15; Length 159;
Best Local Similarity 68.6%; Pred. No. 4.2e-07;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1249.17 Seconds
(without alignments)
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Title: US-10-724-532-6
Perfect score: 135
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_sy:*
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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.4	38.8	858	4	RABPHLAM2
2	52.4	38.8	2841	4	OCPEHAM
3	50.8	37.6	159	6	BD247907
4	50.8	37.6	159	6	BD247911
5	50.8	37.6	159	6	AR302003
6	50.8	37.6	159	6	AR302007
7	50.8	37.6	159	6	AX040487
8	50.8	37.6	159	6	AX040491
9	50.8	37.6	737	4	SSRLB
10	50.2	37.2	159	10	SS5853
11	50.2	37.2	386	10	SS5849
12	50.2	37.2	701	10	RNPPLAMB
13	50.2	37.2	1786	10	RATPHOLA02
14	50.2	37.2	223728	2	AC097906
15	50.2	37.2	231910	2	AC128365
16	47.6	35.3	130240	5	BX276081
17	47.6	35.3	133901	5	BX537355
18	47	34.8	648	10	BC061097
19	47	34.8	940	10	S46792

20	47	34.8	79895	2	AC100317	Mus muscu
21	47	34.8	177018	2	AC099716	Mus muscu
22	46.6	34.5	3312	5	CHKPLB	Chicken car
23	46.6	34.5	3423	5	CHKPLB2	Chicken pho
24	46	34.1	306	6	C0447405	Sequence
25	46	34.1	323	9	HDMPPLAM	Human phosph
26	46	34.1	480	6	AX894936	Sequence
27	46	34.1	480	6	BD030469	Sequence
28	46	34.1	980	9	HSPLB2	AF177764 Homo sapi
29	46	34.1	1635	6	C0718671	Sequence
30	46	34.1	1635	6	AX329653	Sequence
31	46	34.1	1635	9	HDMPPLAM	Human phosph
32	46	34.1	1691	9	BC005269	Homo sapi
33	46	34.1	60797	2	AL355356	Homo sapi
34	46	34.1	66092	2	AL136974	Homo sapi
35	46	34.1	150290	9	HS00914	Human DNA
36	44.4	32.9	314	4	AY514751	Canis fam
37	44.4	32.9	832	4	DOGPHL	Canine card
38	44.4	32.9	832	4	DOGPLBA	Dog phospho
39	44.4	32.9	2614	4	CPPLHX	Dog phospho
40	44.2	32.7	315	6	AR121629	Sequence
41	36.2	26.8	147419	9	HS338911	Human DNA
42	35.6	26.4	184450	2	AC116417	Mus muscu
43	35.2	26.1	209299	5	AC145916	Gallus ga
44	35	25.9	5702	6	CQ719769	Sequence
45	35	25.9	6481	6	AR339585	Sequence

ALIGNMENTS

RESULT 1	RABPHLAM2	858 bp	DNA	linear	MM 27-APR-1993
LOCUS	RABPHLAM2				
DEFINITION	Rabbit phospholamban gene, partial exon 2.				
ACCESSION	M63601				
VERSION	M63601.1 GI:165636				
KEYWORDS	phospholamban.				
SEGMENTS	2 of 3				
SOURCE	Oryctolagus cuniculus (rabbit)				
ORGANISM	Oryctolagus cuniculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
AUTHORS	Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and MacLennan,D.H.				
TITLE	Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6				
JOURNAL	J. Biol. Chem. 266 (18), 11669-11675 (1991)				
MEDLINE	91268032				
PUBMED	1828805				
COMMENT	Original				
FEATURES	source text: Rabbit DNA.				
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	/db_xref="taxon:9986"				
	/tissue_id="rabbit genomic"				
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	/product="phospholamban"				
	428..858				
	/product="phospholamban"				
	/number=2				
	524..682				
	/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"				
	/codon_start=1				
	/product="phospholamban"				
	/protein_id="AA31445.1"				
	/db_xref="GI:165639"				
	/translation="MEKQVLTGSAIRRASTIEMPOQARQNLQNLFINPCLILCLLL				
	ICITVIMLL"				
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Query Match 38.8%; Score 52.4; DB 4; Length 858;
Best Local Similarity 69.6%; Pred. No. 1.1e-05;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Db 17 AGAGCATGAGATGAATGCAATTCAGCAGAGCGCATGAGATCAGACAAAAGCAATG 76
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678 AGAAGCATGAGCATGATCAGATCAGCAGAGACATATCAAGATGAGACAGAAATTGATA 619
|||

Qy 77 AAAGCATCTGAGAGTCTGCGCTGAGCGCTGAGCGCTTCTCTCA 118
|||
618 AATAGCTTCTGAGGTTTGAAGCTTGTGAGGCAATTTCA 577
|||

RESULT 2
LOCUS OCPHAM/c 2841 bp mRNA linear MAM 24-JUL-1992
DEFINITION O.cuniculus mRNA for phospholamban.
ACCESSION Y00761
VERSION Y00761.1 GI:1661
KEYWORDS phospholamban.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2841)
AUTHORS Fujii, J., Lytton, J., Tada, M. and MacLennan, D.H.
TITLE Rabbit cardiac and slow-twitch muscle express the same
JOURNAL phospholamban gene
MEDLINE PERS Lett. 227 (1), 51-55 (1988)
PUBMED 8811222
FEATURES
source 2962883
location/Qualifiers
1..2841
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"
/protein_id="CA68730.1"
/db_xref="GI:1662"
/db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKQVYLRSAIRASTIEMPOQARONLQNLFINFCLILCLLL
ICIIIVMLL"

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Query Match 38.8%; Score 52.4; DB 4; Length 2841;
Best Local Similarity 69.6%; Pred. No. 1.3e-05;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 17 AGAGCATGAGATGAATGCAATTCAGCAGAGCGCATGAGATCAGACAAAAGCAATG 76
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Db 332 AGAAGCATGAGCATGATCAGATCAGCAGAGACATATCAAGATGAGACAGAAATTGATA 273
|||

Qy 77 AAAGCATCTGAGAGTCTGCGCTGAGCGCTGAGCGCTTCTCTCA 118
|||
272 AATAGCTTCTGAGGTTTGAAGCTTGTGAGGCAATTTCA 231
|||

RESULT 3
LOCUS BD247907/c 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE
Sus sp.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 159)

AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV

COMMENT
OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C1201/42, C12N15/09, C12Q1/02, C12N15/00
CC Method for screening compounds
FH Location/Qualifiers
FT source 1..159
/organism="Sus sp. (pig)".

FEATURES
source
location/Qualifiers
1..159
/organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"

ORIGIN
Query Match 37.6%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.1e-05;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 17 AGAGCATGAGATGAATGCAATTCAGCAGAGCGCATGAGATCAGACAAAAGCAATG 76
|||
Db 155 AGAAGCATGAGCATGATGCAATTCAGCAGAGCGCATTTAGATGAGACGAAATTGATA 96
|||

Qy 77 AAAGCATCTGAGAGTCTGCGCTGAGCGCTGAGCGCTTCTCTCA 118
|||
Db 95 AATAGCTTCTGAGGTTTGAAGCTTGTGAGGCAATTTCA 54
|||

RESULT 4
LOCUS BD247911/c 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE
ORGANISM
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV

COMMENT
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG P18 CDNA FH
FH Key
FT source 1..159
/organism="Artificial Sequence".

FEATURES
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location/Qualifiers
1..159
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ORIGIN
Query Match 37.6%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.1e-05;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hyperenstion, diabetes, Darter-White disease and Brody's disease
XX
SQ Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;
Query Match 37.6%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 6.9e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 17 AGAGCATGATGATTAATGCAATTCAGCAGGAGGAGATGAGATTCAGCAAAAGCAATG 76
DB 155 AGAAGCATGACAGATGATGATCAATGCAAGAGGATATTAGATGAGACAGAAATTGATA 96
OY 77 AAAGCATTCGAGGATTCGCTGCGCTGAGGAGGCTTCTCTCA 118
DB 95 AATAGCTTCTGAAAGGTTTGACGTCTTGTGAGGCAATTTC 54

RESULT 2
ADBS3082/C
ID ADBS3082 standard; DNA; 701 BP.
XX
AC ADBS3082;
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.
XX
DE toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
PN MO2003065993-A2.
XX
PD 14-AUG-2003.
XX
PE 04-FEB-2003; 2003MO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-036534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elshof M;
XX
DR WPI; 2003-731472/69.
XX
XX
XX Determining if a compound induces a toxic effect on a tissue or cell, for
XX identifying hepatotoxic compounds, comprises comparing a gene expression
XX profile of a tissue or cell sample to a database of Tox mean and non-Tox
XX mean values.
PS Claim 44; SEQ ID NO 3624; 874bp; English.

XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 701 BP; 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;
Query Match 37.2%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 1.7e-05;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
OY 16 CAGAGCATGACGATTAATGCAATTCAGCAGGAGGAGATGAGATTCAGCAAAAGCAAT 75
DB 329 CAGAGCATGACGATTAATGCAATTCAGCAGGAGGAGATTCAGCAAAAGCAATTCAT 270
OY 76 GAAAGCATTCGAGGATTCGCTGCGCTGAGGAGGCTTCTCTCA 118
DB 269 AAGAGGTTCTGAGGTTCTGACGCGCTTGTGCGGCAATTTC 227

RESULT 3
ADR97285/C
ID ADR97285 standard; DNA; 159 BP.
XX
AC ADR97285;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human phospholamban polymorphism fragment DNA.
XX
KM ds; human; phospholamban; polymorphism; cardiovascular disease.
XX
OS Homo sapiens.
XX
PN US2004191802-A1.
XX
PD 30-SEP-2004.
XX
PR 22-OCT-2003; 2003US-00691412.
XX
PR 22-OCT-2002; 2002US-0420295P.
XX
PA (KRAN/) KRANTAS E. G.
XX (HAGH/) HAGHIGHT K.
XX
PI Krantias EG, Haghighi K;
XX
DR WPI; 2004-699841/67.
XX
XX
XX Phospholamban polymorphism assessment in individual, for determining risk
XX for developing cardiovascular disease, by comparing analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence.
XX
PS Claim 15; SEQ ID NO 1; 15bp; English.
XX
XX
XX The invention relates to a method of phospholamban polymorphism
XX assessment in an individual which comprises comparing the analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence to determine whether the individual carries a
XX phospholamban polymorphism. The methods and phospholamban polymorphism
XX fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1691.67 Seconds
(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-6

Perfect score: 135
Sequence: 1 ctctctctctcgcagcagga.....tcacgcatcagcttctctc 135

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hnc:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
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2	50.8	37.6	702	5	BX922974 BX922974
3	50.8	37.6	724	5	BX674983 BX674983
4	50.8	37.6	740	5	BX924154 BX924154
5	50.8	37.6	758	5	BX923697 BX923697
6	50.8	37.6	811	7	CK449263 CK449263
7	50.2	37.2	179	2	BE113353 BE113353
8	50.2	37.2	377	2	BF547322 BF547322
9	50.2	37.2	417	1	AI322542 AI322542
10	50.2	37.2	439	2	BE115006 BE115006
11	50.2	37.2	449	2	BF394968 BF394968
12	50.2	37.2	449	2	BE098177 BE098177
13	50.2	37.2	451	4	BE128891 BE128891
14	50.2	37.2	454	2	BE099930 BE099930
15	50.2	37.2	476	2	BF552528 BF552528
16	50.2	37.2	480	7	CR471116 CR471116
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18	50.2	37.2	498	1	AI603160 AI603160
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31	50.2	37.2	719	7	CK356296 CK356296
32	50.2	37.2	731	7	CK357243 CK357243
33	50.2	37.2	737	7	CK357232 CK357232
34	50.2	37.2	738	7	CK355359 CK355359
35	50.2	37.2	738	7	CK357123 CK357123
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37	50.2	37.2	744	7	CK357747 CK357747
38	50.2	37.2	745	7	CK355314 CK355314
39	50.2	37.2	745	7	CK356371 CK356371
40	50.2	37.2	748	7	CK359219 CK359219
41	50.2	37.2	754	7	CK355445 CK355445
42	50.2	37.2	758	7	CK355453 CK355453
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44	50.2	37.2	762	7	CK359188 CK359188
45	50.2	37.2	764	7	CK357447 CK357447

ALIGNMENTS

RESULT 1
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LOCUS BX669692 Sus Scrofa library (secac) Sus scrofa cDNA clone
DEFINITION scac00281.c.02 5prim, mRNA sequence.
ACCESSION BX669692
VERSION BX669692.1 GI:37979481
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
Auteurs Bonnet, A., Tosser-Klopp, G., Benne, F., Gabau, C., Villegier, S., Soares, M., Bonaldi, F. and Hately, F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenauporte@jouy.inra.fr to obtain the chromatogram of this sequence.
Plate: 0028 row: c column: 2.

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/clone_lib="Sus Scrofa library (secac)"
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ORIGIN
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37.6% Score 50.8; DB 5; Length 381;

Best Local Similarity 68.6%; Pred. No. 0.00029;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Oy 77 AAAGCATTCTGAGGTTCTGCCTGGCCGTAGGCCCTTCTCA 118
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DEFINITION	Scrofa library (scan)	Scrofa CDNA clone			
	scan0013d.j.14	5prim.	mRNA sequence.		

ACCESSION	BX922974	GI:41139822
VERSION	BX922974.1	
KEYWORDS	EST.	
SOURCE	Sus scrofa	(pig)
ORGANISM	Sus scrofa	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus. 1 (bases 1 to 702)
Bonner, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S., Soares, M., Bonaldo, F. and Hately, F.
A pig Normalized Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G

Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel.: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence. Plate: 0013 row: j column: 14.

FEATURES	Location/Qualifiers
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skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbourethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder."

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ORIGIN

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RESULT 3

EX674983/c	BK674983	724 bp	mRNA	linear	EST 07-MAY-2004
LOCUS	BK674983				
DEFINITION	BK674983 Sus Scrofa library (scac) Sus scrofa cDNA clone				
	gcac00391.h.23 5prim, mRNA sequence.				

ACCESSION	BX674983
VERSION	BX674983.1
KEYWORDS	GI:38008935 EST.

SOURCE ORGANISM	Sus scrofa (pig)
Sus scrofa	
Sus scrofa	

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE	AUTHORS
1 (bases 1 to 724)	Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,

TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G

Genétique Animale
Institut National de la Recherche Agronomique
Chemin de Bordeaux - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5 61 28 51 14
Fax: 33 (0) 5 61 28 53 08
Email: cosser@couleuse.inra.fr
Sequence cleaner of vector, adaptor and repetitions. Contact
at siemensupport@jouy.inra.fr to obtain the chromatogram of the
sequence.
Plate: 0039, row: h, column: 23.

FEATURES
source

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organism="Sus scrofa"
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brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbourethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

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ORIGIN

Query Match	37.6%	Score 50.8;	DB 5;	Length 724;
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Oy 77 AAAGCATTCTGAGGTTCTGCCTGGCCGTAGGCCCTTCTCA 118
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RESULT 4

LOCUS	740 bp	mrna	linear	EST 07-MAY-2004
DEFINITION	BX924154	Sus Scrofa library (scan)	Sus scrofa cDNA clone	
	BX924154	scan001d.f.23	5prim. mrna sequence.	

VERSION	BX924154.1	GI:41141002
KEYWORDS	EST.	
SOURCE	Sus scrofa (pig)	

ORGANISMS

REFERENCE
1 (bases 1 to 740)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

AUTHORS Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.

FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT ADDITION NUMBER: USC/00/EA0 873P

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PIG CDNA
US-09-549-872B-13

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Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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RESULT 3

US-09-513-999C-10799/C
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10799
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799

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Best Local Similarity 65.7%; Pred. No. 8.4e-06;
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RESULT 4
US-09-949-016-1439/C
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439

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Best Local Similarity 65.7%; Pred. No. 1.5e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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RESULT 5

US-09-949-016-13181/C
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13181
; LENGTH: 16062
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181

Query Match 34.1%; Score 46; DB 4; Length 16062;
Best Local Similarity 65.7%; Pred. No. 4.2e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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DB 12762 AGAAGCATCAGATGATCAATCAGCAGAGCGATATTAAGATGACAGAAATTGATA 12703
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QY 77 AAAGATTCTGAGGTTCTGCTGGCCCTGAGGCTTCTCTCA 118
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RESULT 6
US-09-124-671-26/C
; Sequence 26, Application US/09124671A

GenCore version 5.1.6
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Run on: July 7, 2005, 09:22:55 ; Search time 325.556 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	108	80.0	108	20	US-10-724-532-4
5	50.8	37.6	159	15	US-10-371-101-9
6	50.8	37.6	159	15	US-10-371-101-13
7	46	34.1	159	19	US-10-691-412-1

C	8	46	34.1	525	10	US-09-918-995-4045	Sequence 4045, Ap
C	9	46	34.1	1635	21	US-09-873-367C-162	Sequence 162, App
C	10	46	34.1	1635	21	US-10-843-641A-162	Sequence 162, App
C	11	45	33.3	45	10	US-09-918-995-3950	Sequence 3950, Ap
C	12	45	33.3	418	10	US-09-918-995-5235	Sequence 5235, Ap
C	13	44.4	32.9	394	10	US-09-918-995-4217	Sequence 4217, Ap
C	14	44.4	32.9	487	10	US-09-918-995-5377	Sequence 5377, Ap
C	15	44.2	32.7	315	20	US-10-815-514-26	Sequence 26, Appl
C	16	44.2	32.7	315	20	US-10-877-930-26	Sequence 26, Appl
C	17	44.2	32.7	315	21	US-10-873-594-26	Sequence 26, Appl
C	18	41.2	30.5	407	10	US-09-918-995-3842	Sequence 3842, Ap
C	19	38	28.1	492	10	US-09-918-995-17377	Sequence 17377, A
C	20	35	25.9	6481	15	US-10-037-970-1076	Sequence 1076, Ap
C	21	35	25.9	10625	9	US-10-117-722-1076	Sequence 1076, Ap
C	22	35	25.9	10625	14	US-09-727-384-5	Sequence 5, Appl
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C	29	33.6	24.9	2419	10	US-09-814-353-20506	Sequence 20506, A
C	30	33.6	24.9	3647	17	US-10-172-118-1260	Sequence 1260, Ap
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C	33	33.6	24.9	3748	9	US-09-925-301-80	Sequence 80, Appl
C	34	33.6	24.9	3925	20	US-10-723-660-4598	Sequence 4598, Ap
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C	37	31.4	23.3	1938	13	US-10-087-192-740	Sequence 740, App
C	38	31.4	23.3	2175	9	US-09-994-485-3	Sequence 3, Appl
C	39	31.4	23.3	2175	9	US-09-832-292-7	Sequence 7, Appl
C	40	31.2	23.1	1137	19	US-10-437-963-88641	Sequence 88641, A
C	41	31.2	23.1	2229	9	US-09-974-300-1671	Sequence 1671, Ap
C	42	30.8	22.8	415	9	US-09-864-761-3536	Sequence 3536, Ap
C	43	30.6	22.7	1591	21	US-10-470-0488-40	Sequence 40, Appl
C	44	30.6	22.7	1591	19	US-10-437-963-78016	Sequence 78016, A
C	45	30.6	22.7	1878	17	US-10-369-493-43089	Sequence 43089, A

ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match 100.0%; Score 135; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 7, 7e-36;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTCTCTCTCTCTGAGCAGGACATGACATTAATGCAATGACGAGGACGATGAGAT	60
Db	135	CTCTCTCTCTCTGAGCAGGACATGACATTAATGCAATGACGAGGACGATGAGAT	76
Qy	61	CAGACAAAAGCATTGAGAGGTTCTGACCTGAGGCTTCTCTCATG	120

Db 75 CAGCAAAAAGCATGAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 16
121 CATAAGCTTTCTCTC 135
15 CATAAGCTTTCTCTC 1

RESULT 2

US-10-724-532-6
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

Query Match 100.0%; Score 135; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 7.7e-36;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTCTCTCTGAGCAGGATGACATTAATGCAATTCAGAGGAGGAGGATGAGAT 60
1 CTCCTCTCTCTGAGCAGGATGACATTAATGCAATTCAGAGGAGGAGGATGAGAT 60
Db 61 CAGCAAAAAGCATGAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 120
61 CAGCAAAAAGCATGAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 120

Qy 121 CATAAGCTTTCTCTC 135
121 CATAAGCTTTCTCTC 135
Db 121 CATAAGCTTTCTCTC 135

RESULT 3

US-10-724-532-3/c
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Query Match 80.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CAGGAGCATGACGATTAATGCAATTCAGAGGAGGAGGATGAGATCAGCAAAAAGCAT 75
16 CAGGAGCATGACGATTAATGCAATTCAGAGGAGGAGGATGAGATCAGCAAAAAGCAT 75

Db 108 CAGGAGCATGACGATTAATGCAATTCAGAGGAGGAGGATGAGATCAGCAAAAAGCAT 49
Qy 76 GAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 123
48 GAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 1

RESULT 4

US-10-724-532-4
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Query Match 80.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CAGGAGCATGACGATTAATGCAATTCAGAGGAGGAGGATGAGATCAGCAAAAAGCAT 75
1 CAGGAGCATGACGATTAATGCAATTCAGAGGAGGAGGATGAGATCAGCAAAAAGCAT 75
Db 76 GAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 123
61 GAAGCATTTCTGGAGGTTCTGCGCTGGAGGCTTCTCTCATG 108

RESULT 5

US-10-371-101-9/c
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Query Match 37.6%; Score 50.8; DB 15; Length 159;
Best Local Similarity 68.6%; Pred. No. 4.2e-07;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;